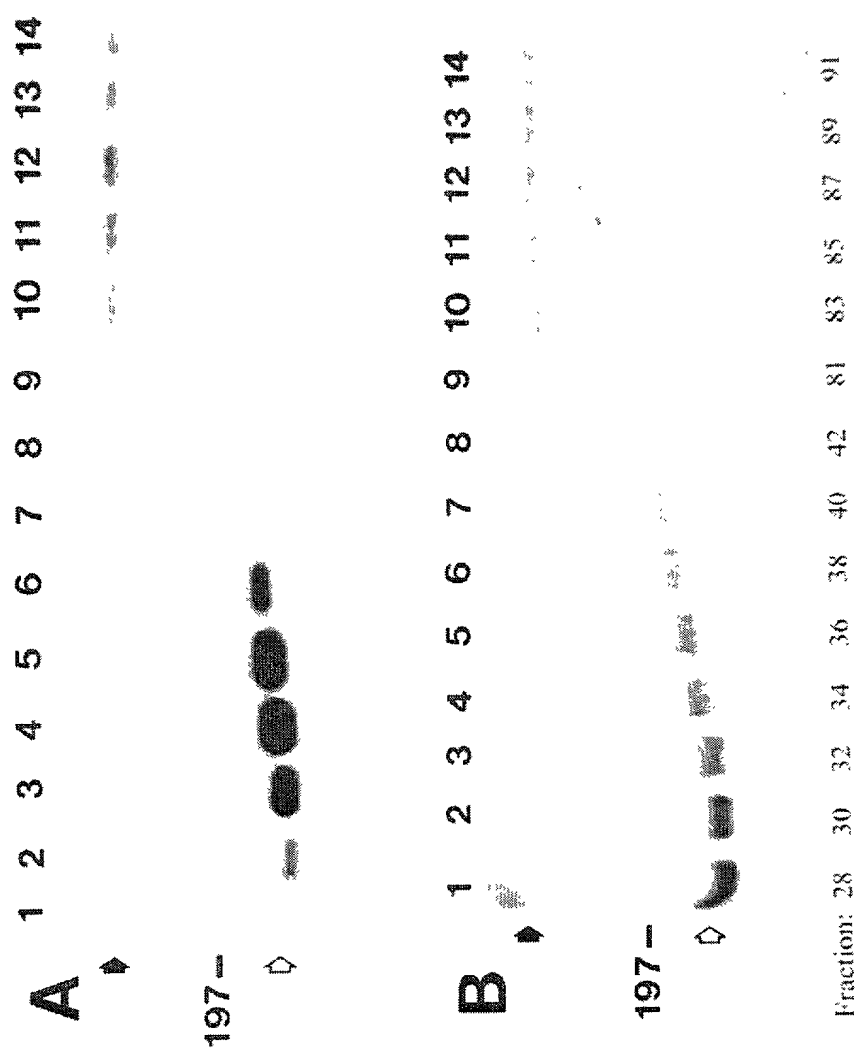


Figure 1



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Figure 2

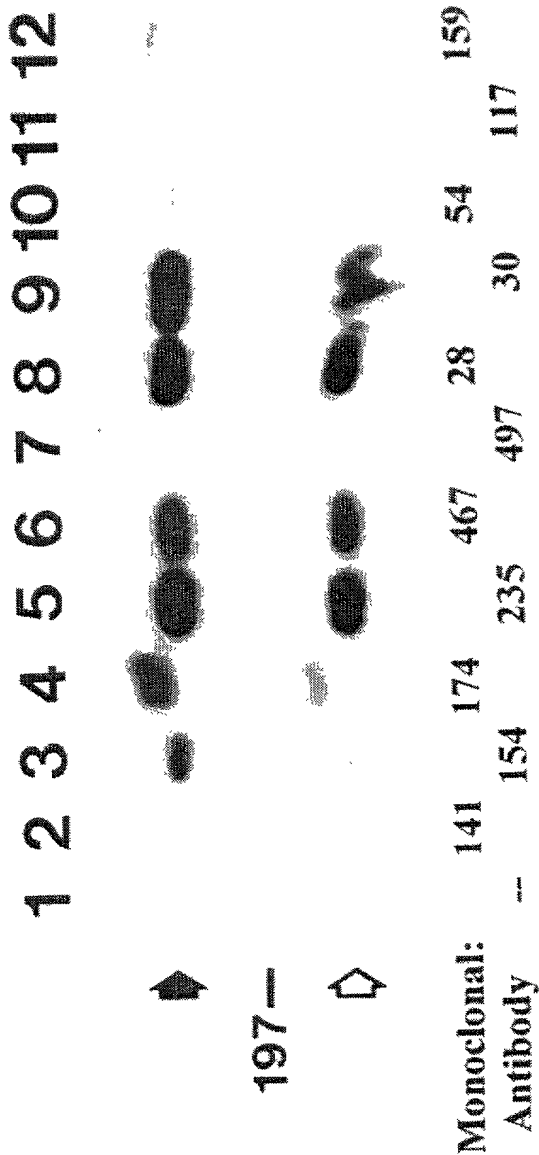


Figure 3

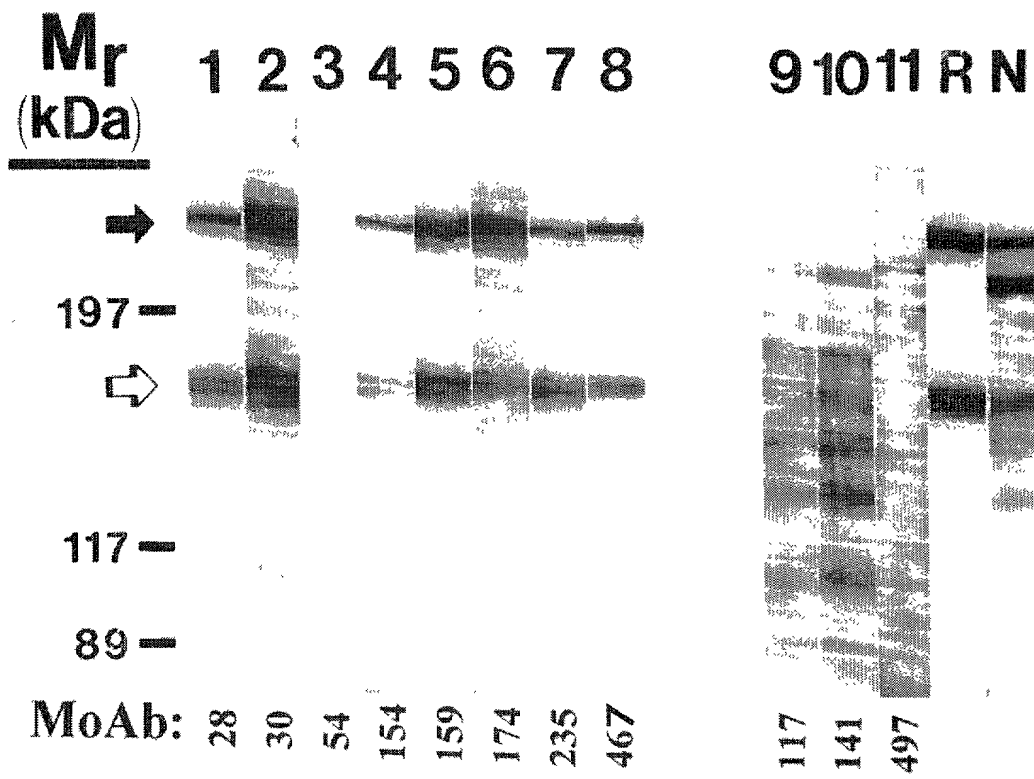
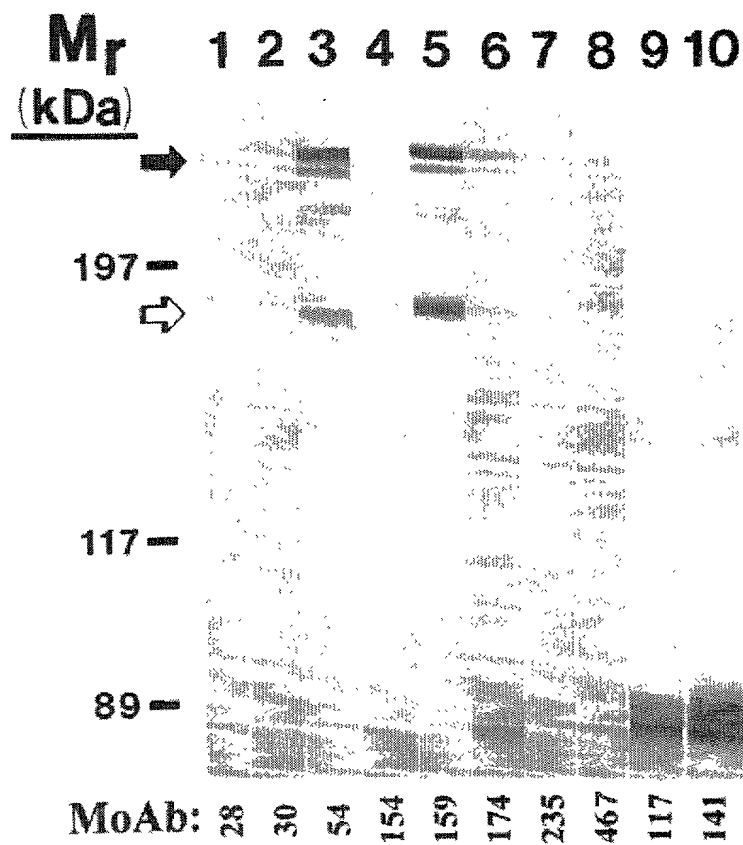
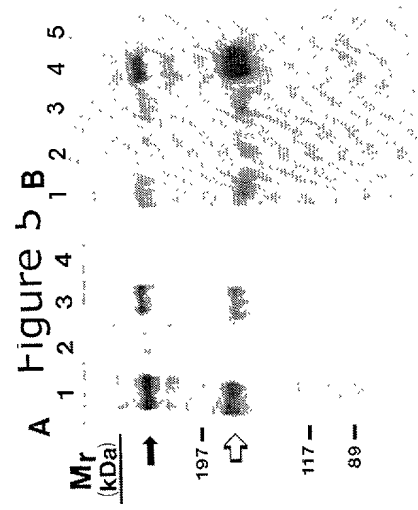


Figure 4



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105240-06624360

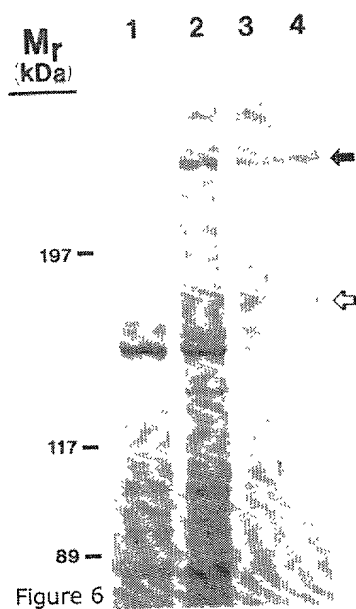
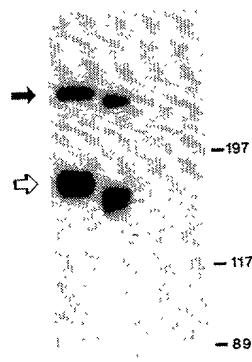


Figure 6

Figure 7 1 2 3 4



PNGaseF:	-	+	-	+
β -ME:	-	-	+	+

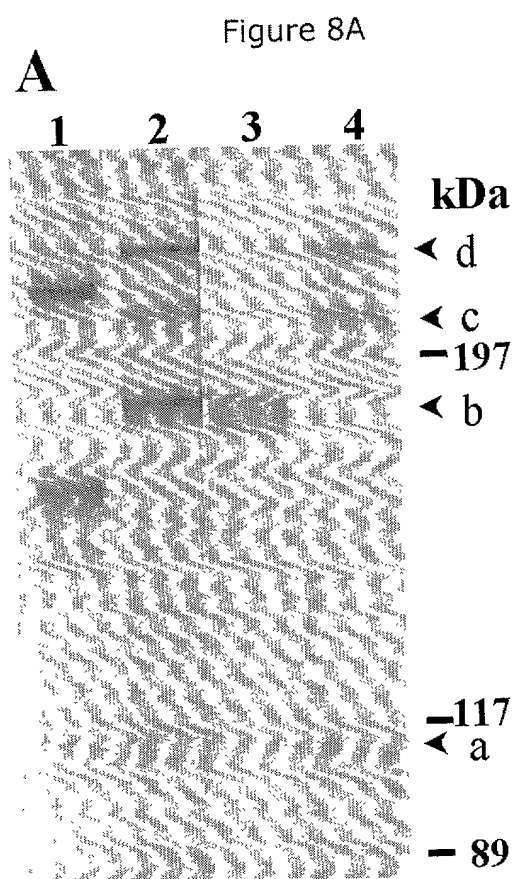
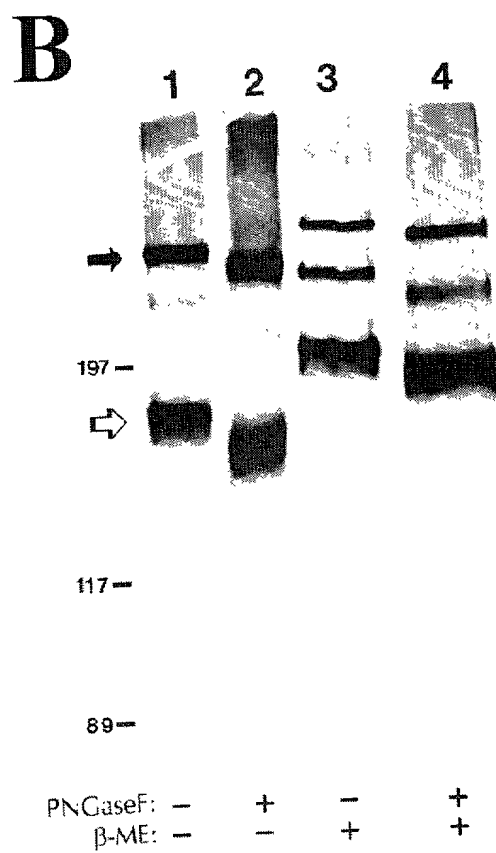
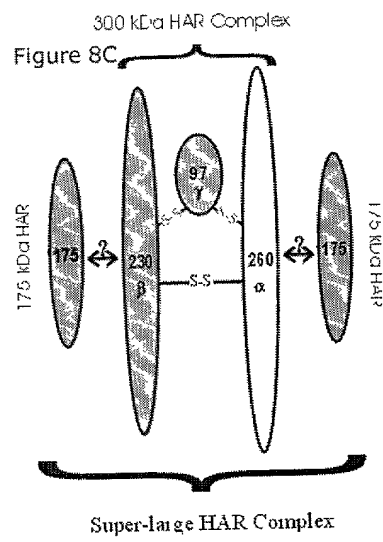


Figure 8B



109240-06624860



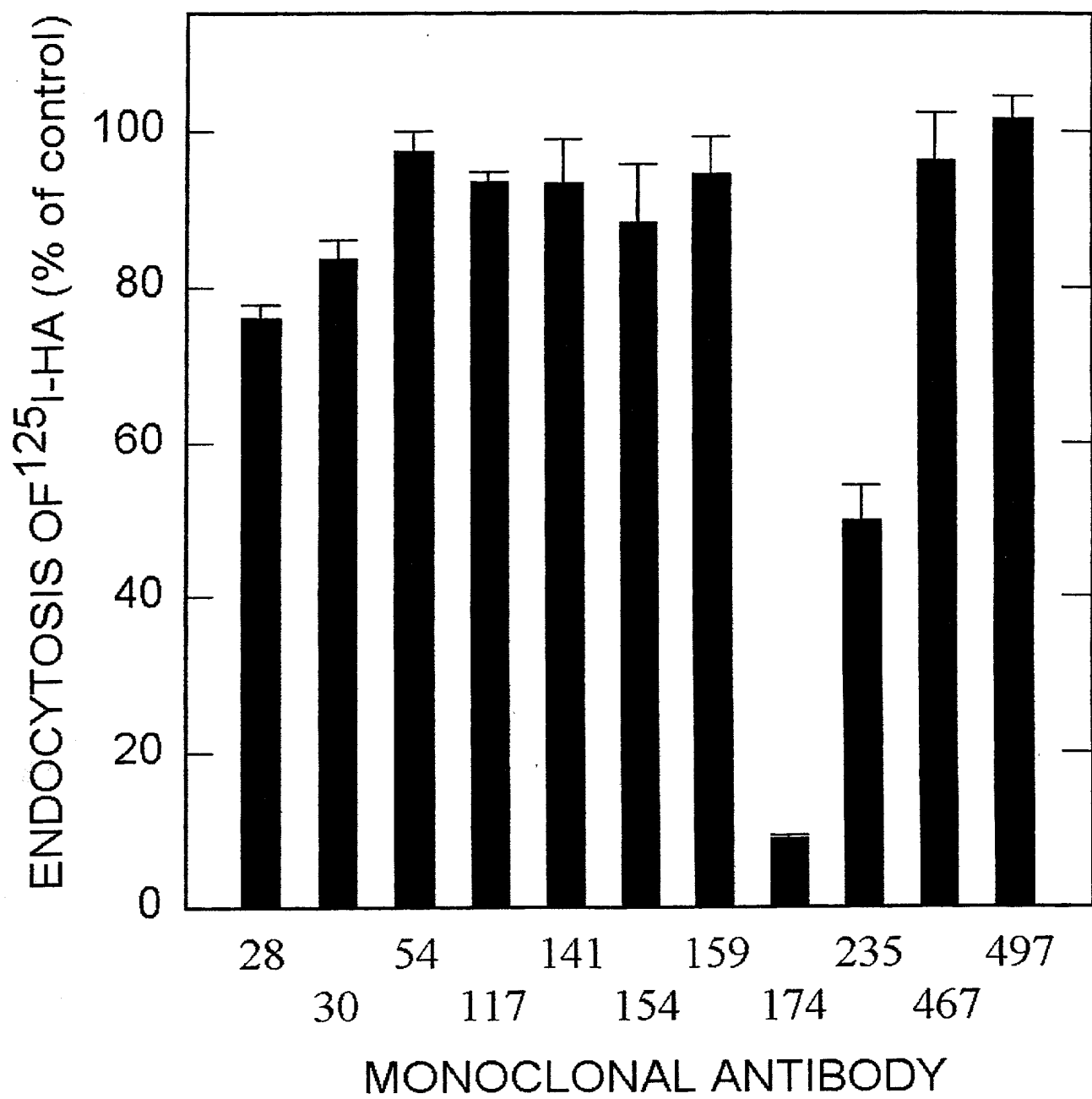
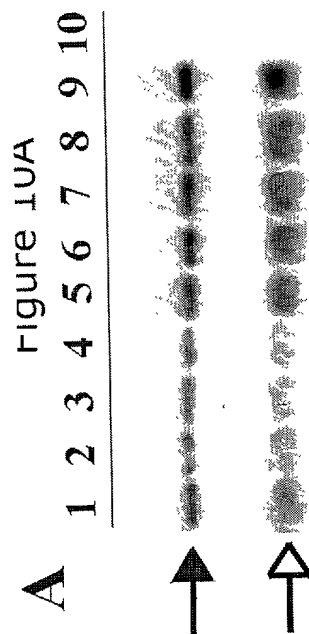


Figure 9



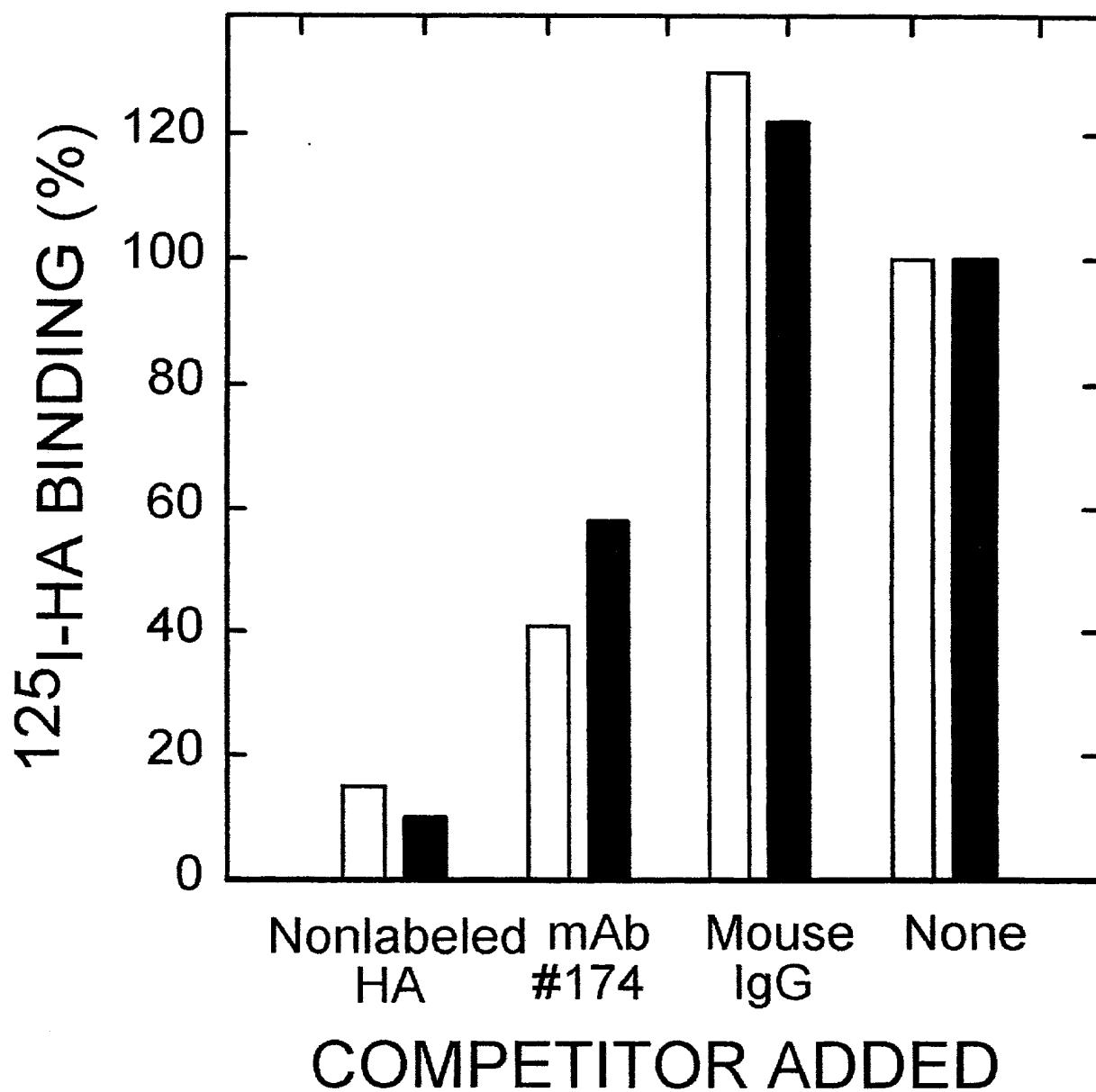


Figure 10B

Figure 11

Antibody Inhibition of HA Endocytosis by HARE in LECs

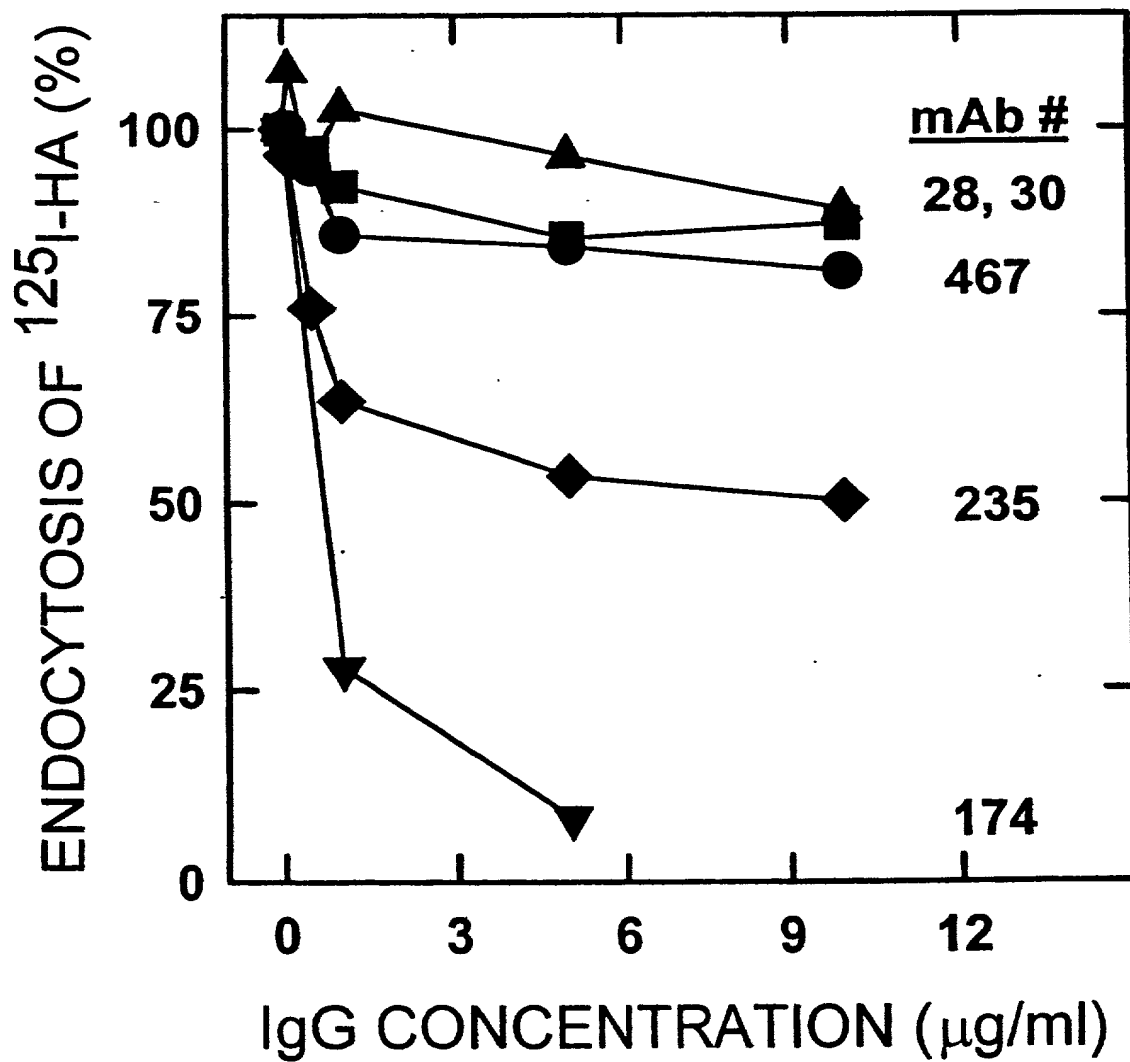


Figure 12

Antibody Inhibition of HA Binding to HARE on LECs is Temperature Dependent

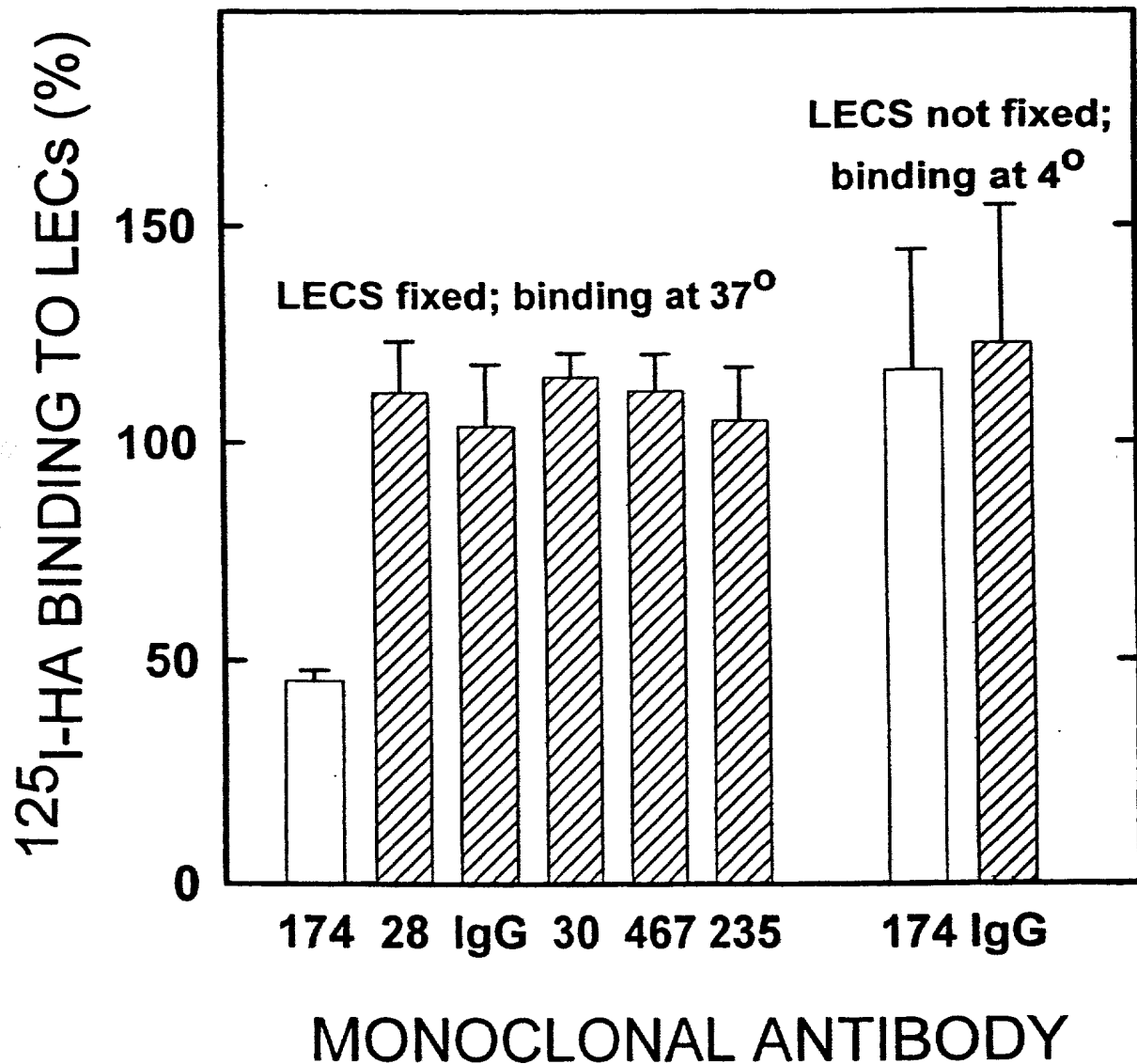
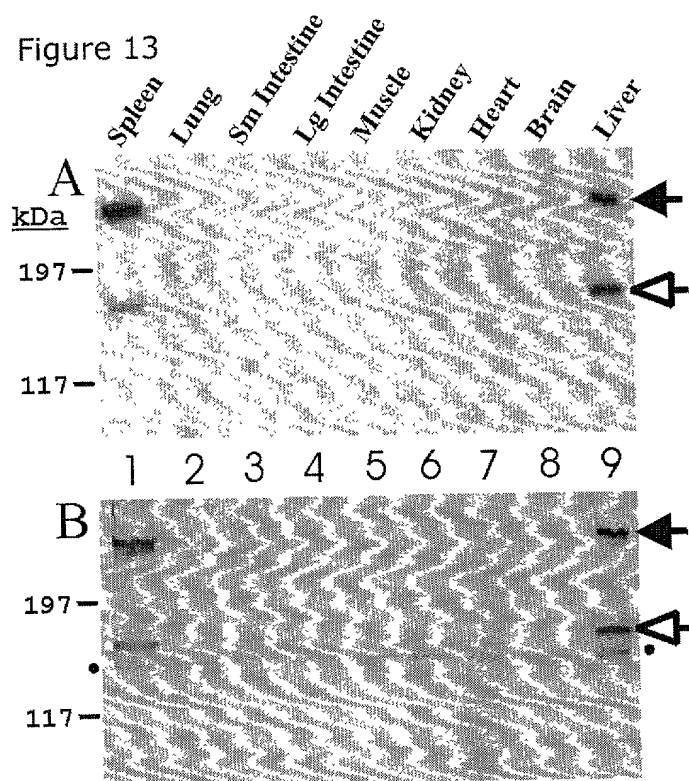


Figure 13



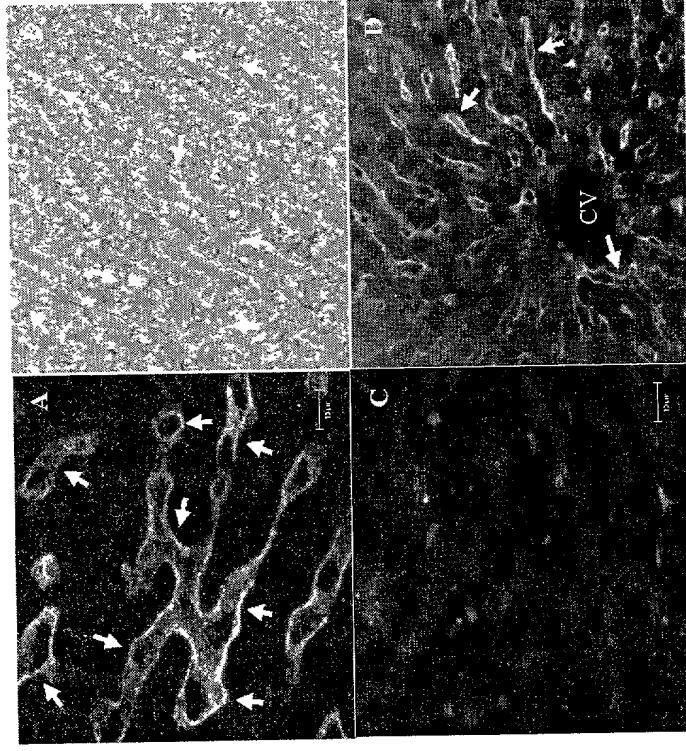


Figure 14

10340-0624350

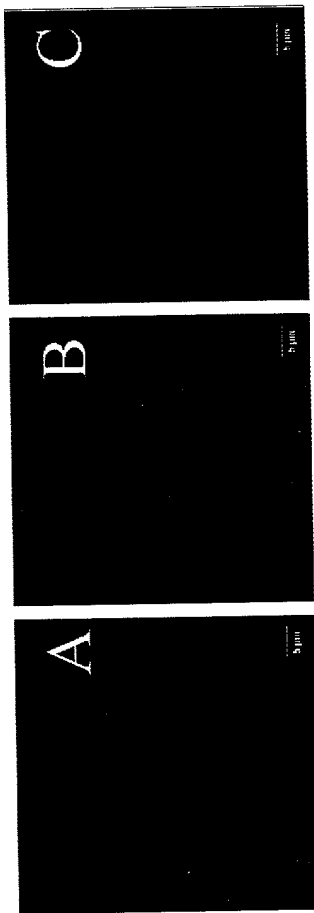


Figure 15

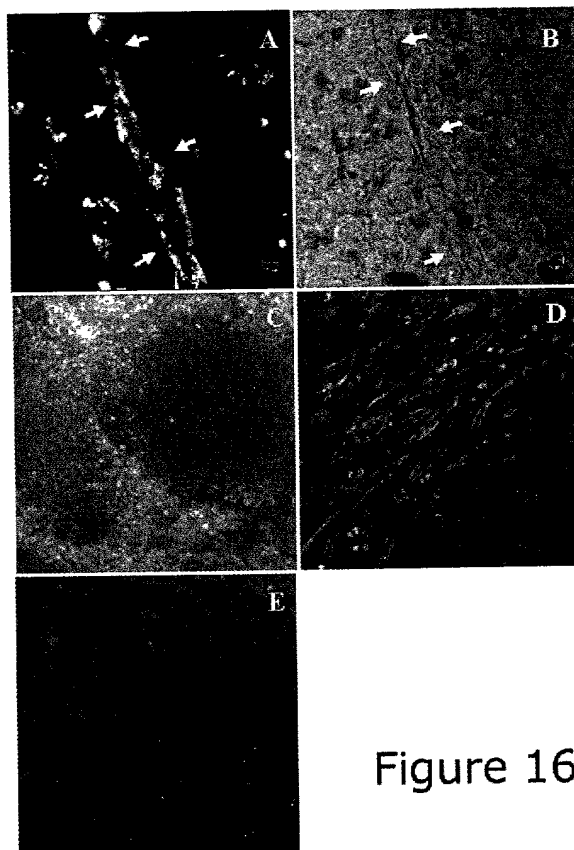


Figure 16

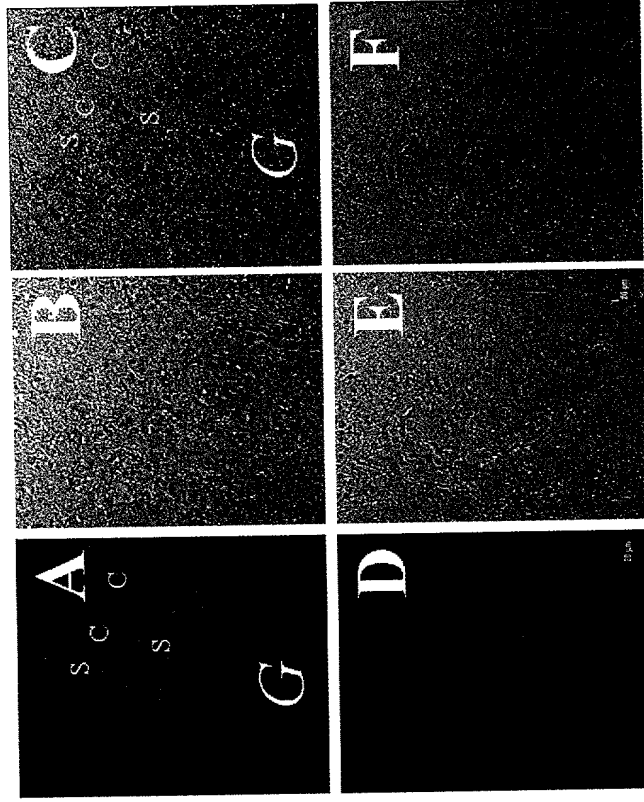
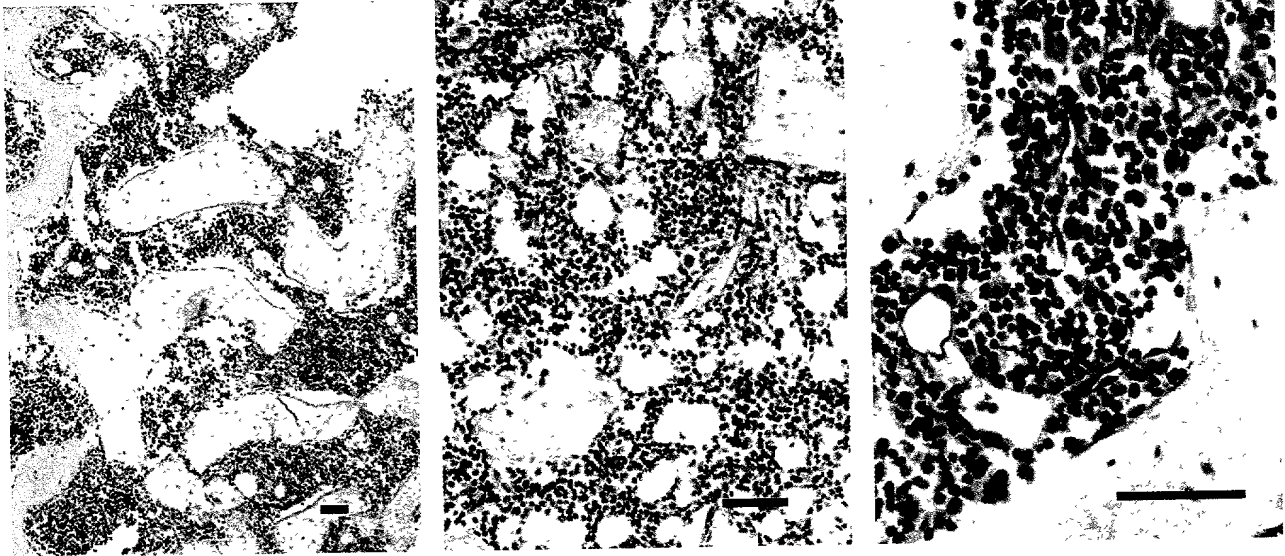


Figure 17

Figure 18

**Immunolocalization of HARE
in Bone Marrow**

Control



Bars = 50 um

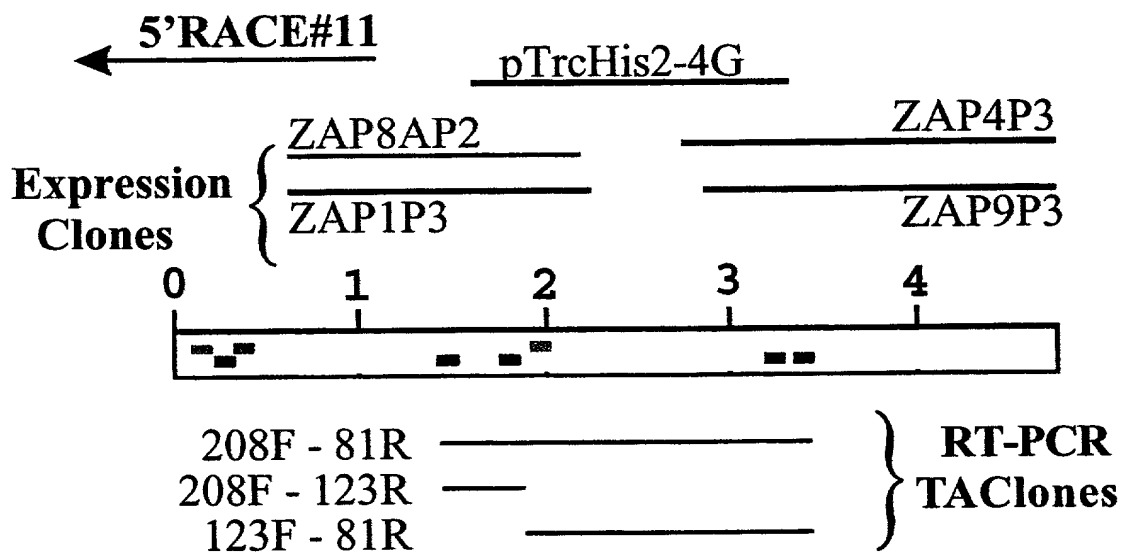
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Figure 20

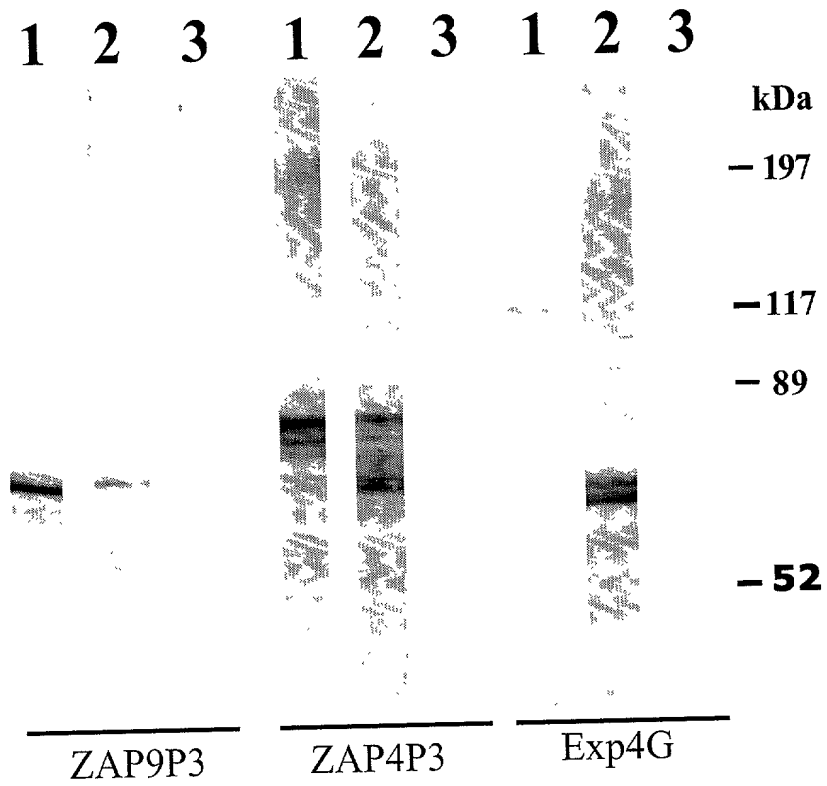


Figure 21

[illegible]

Figure 22

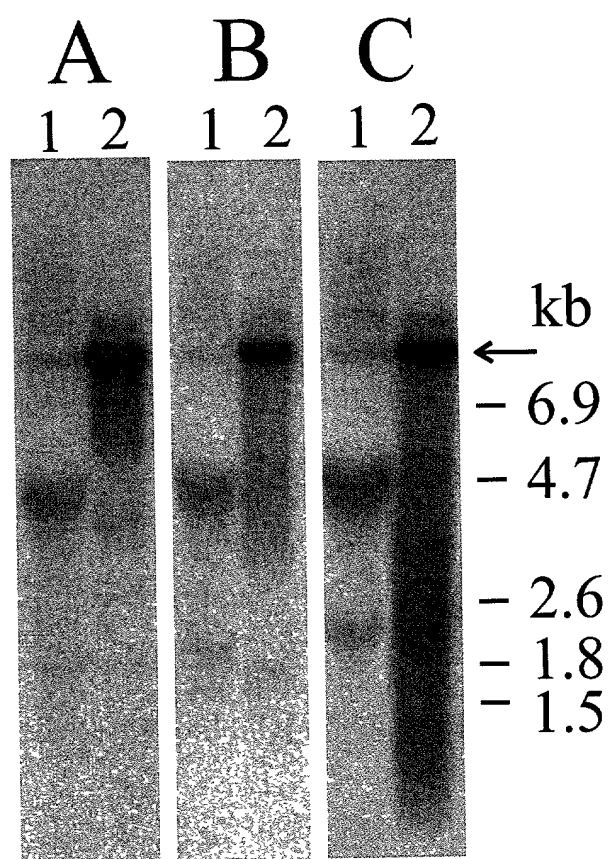


Figure 23

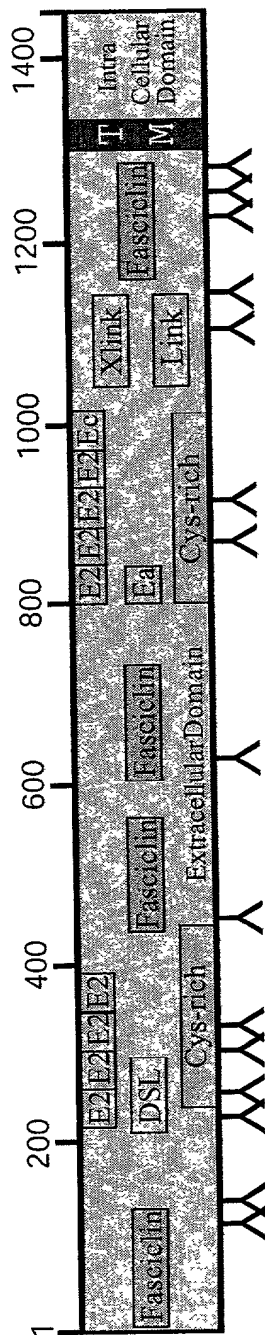


Figure 24

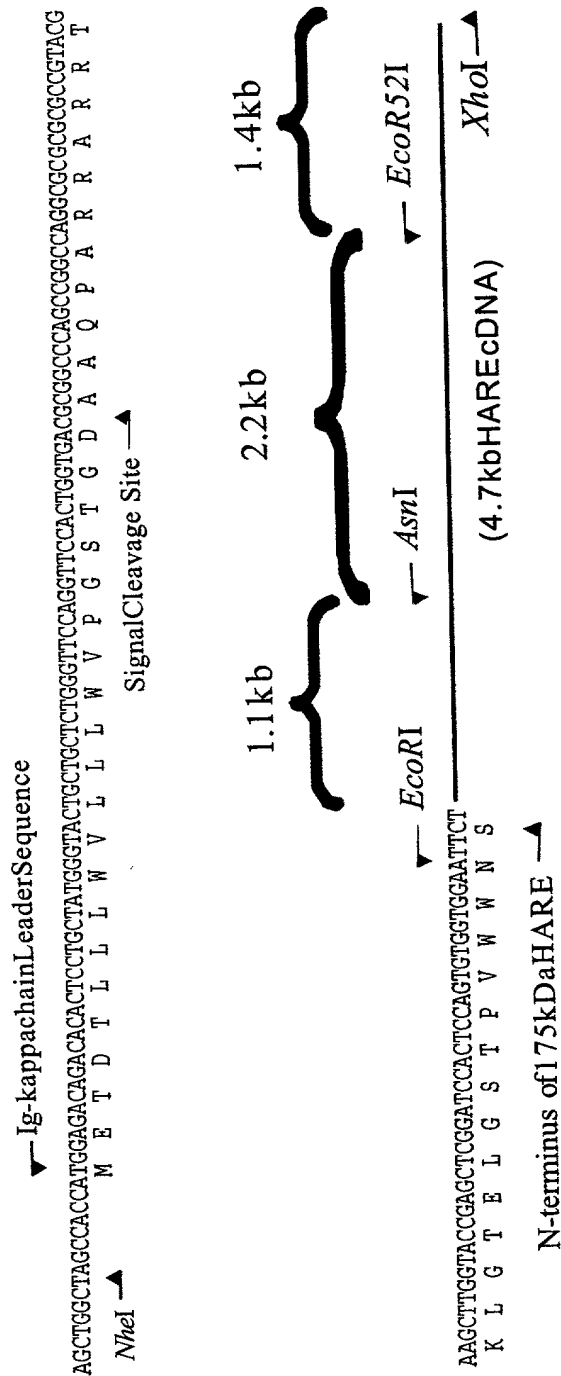
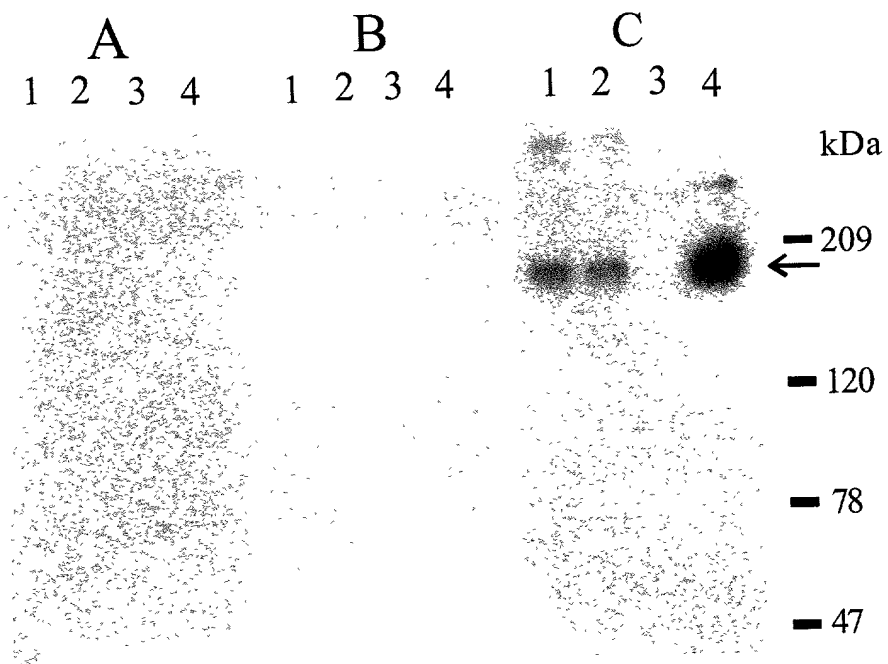


Figure 25

Autoradiography



Western Blot

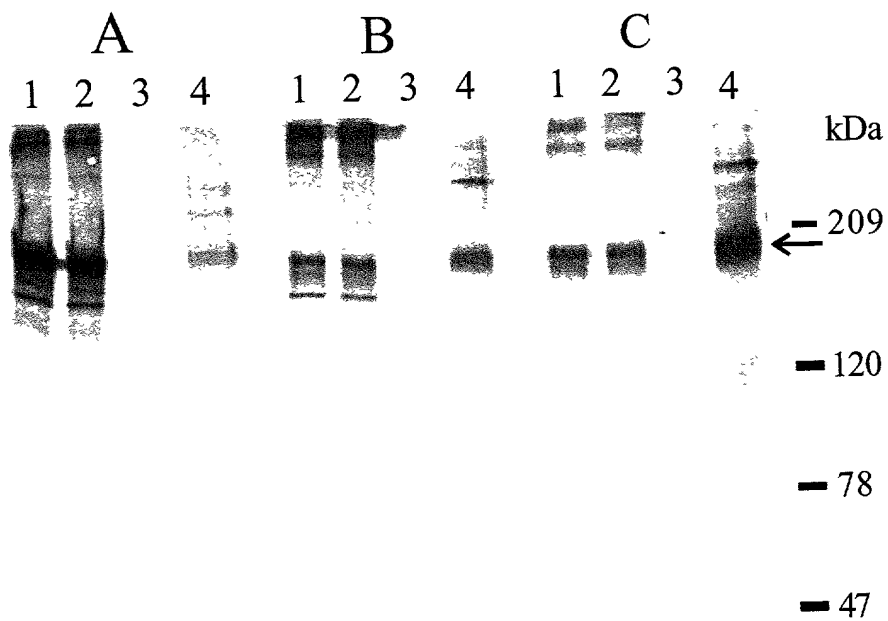


Figure 26

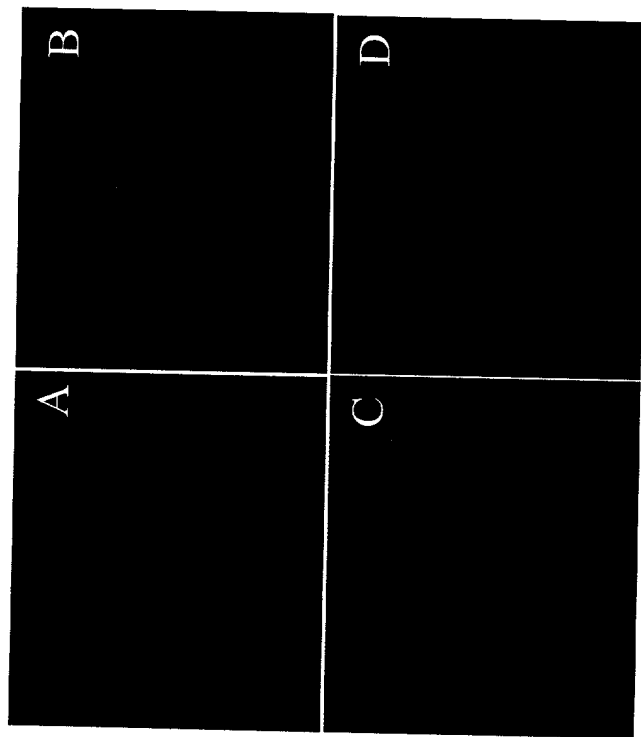


Figure 27A

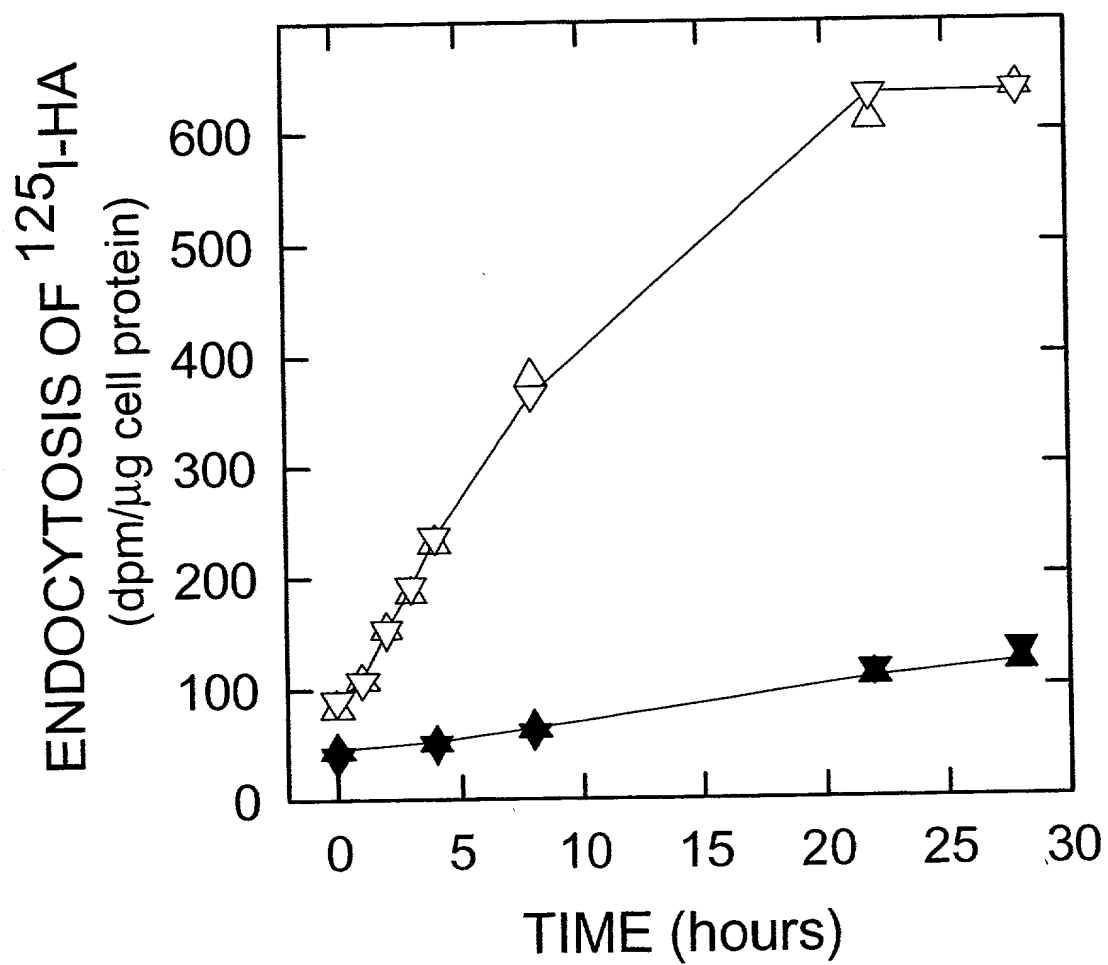


Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

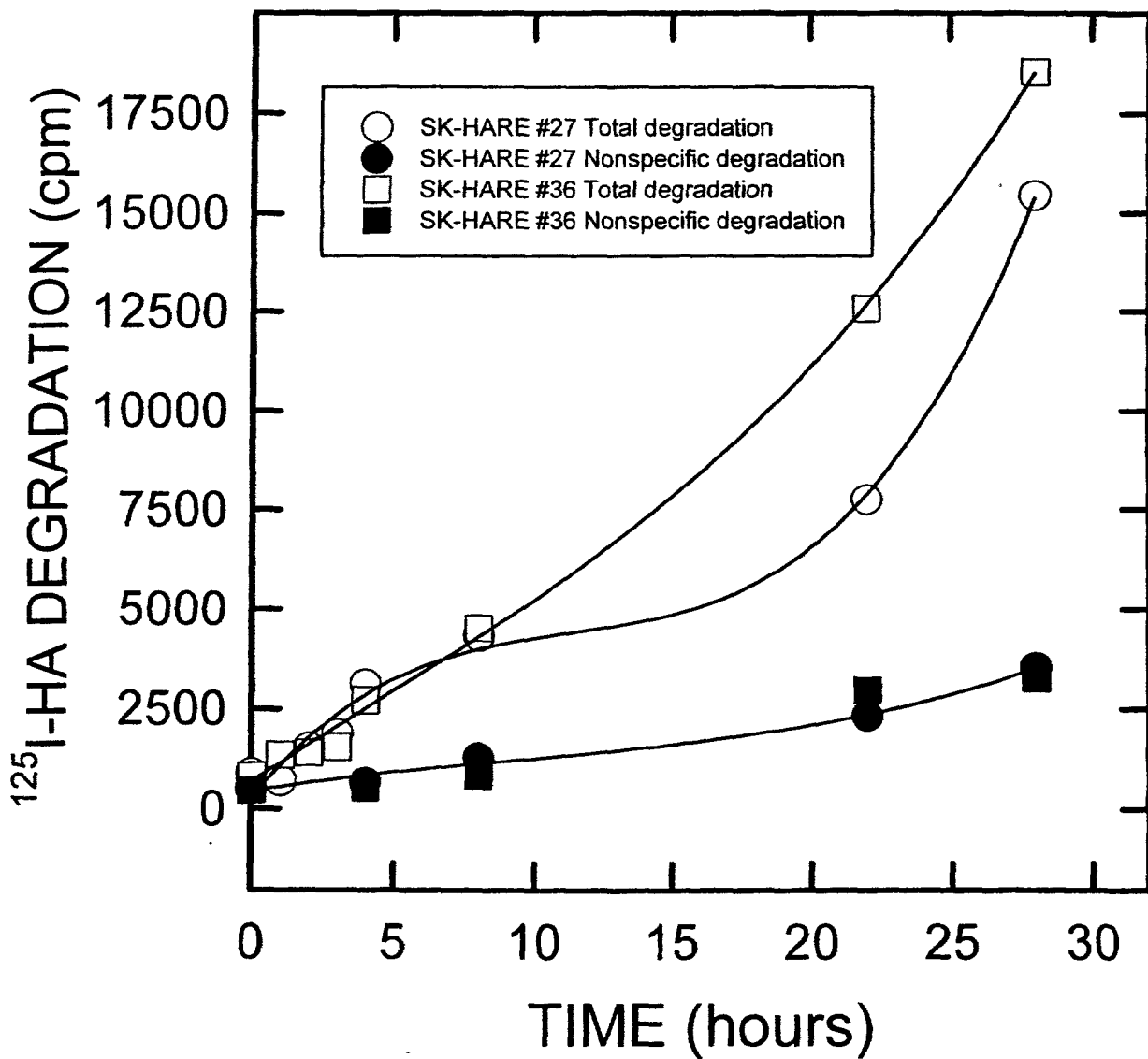


Figure 27C

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells

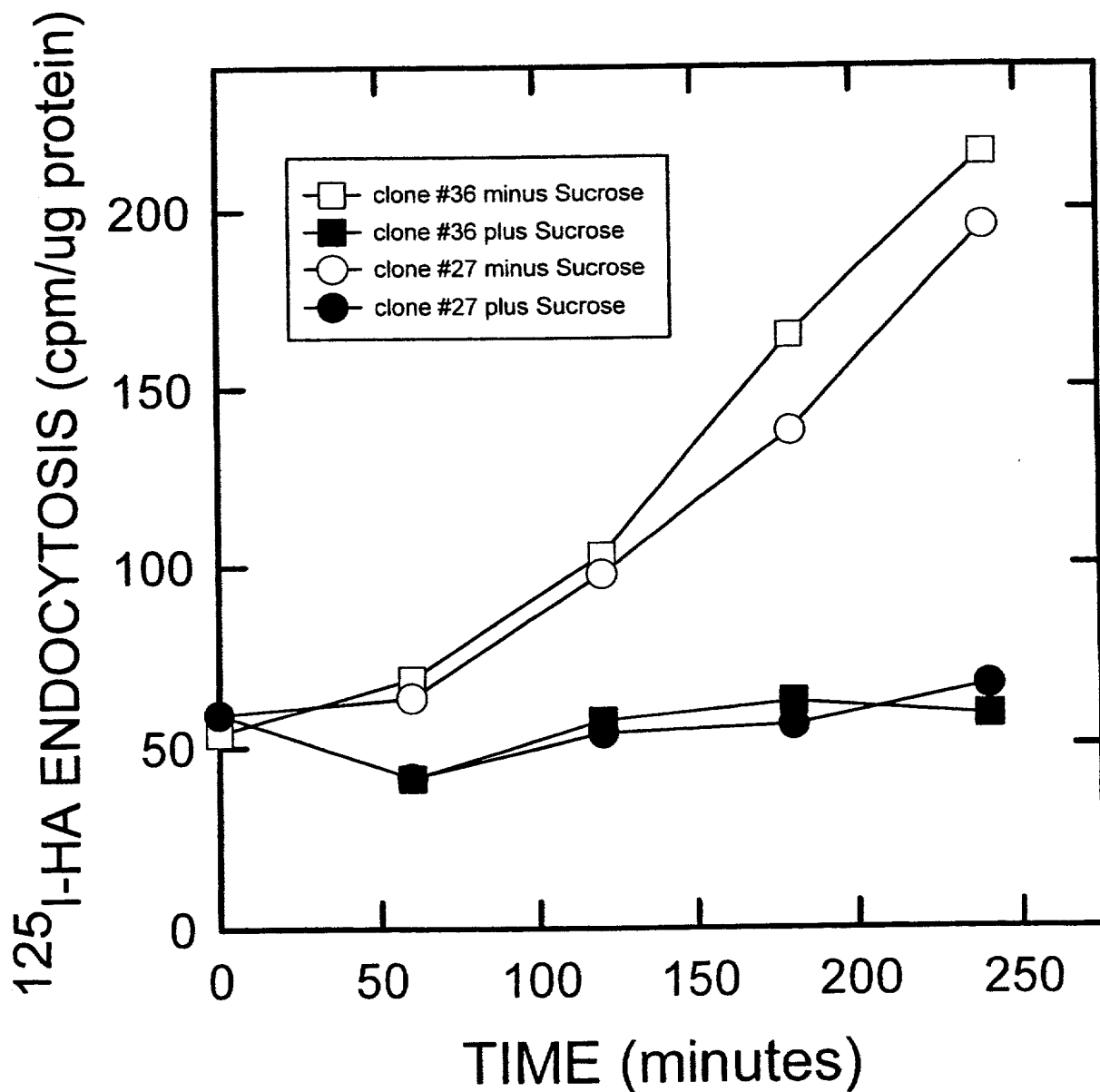


Figure 27D

**Specific monoclonal antibodies against HARE
inhibit HA endocytosis in SK-Hep1
transfectants expressing the 175-kDa HARE**

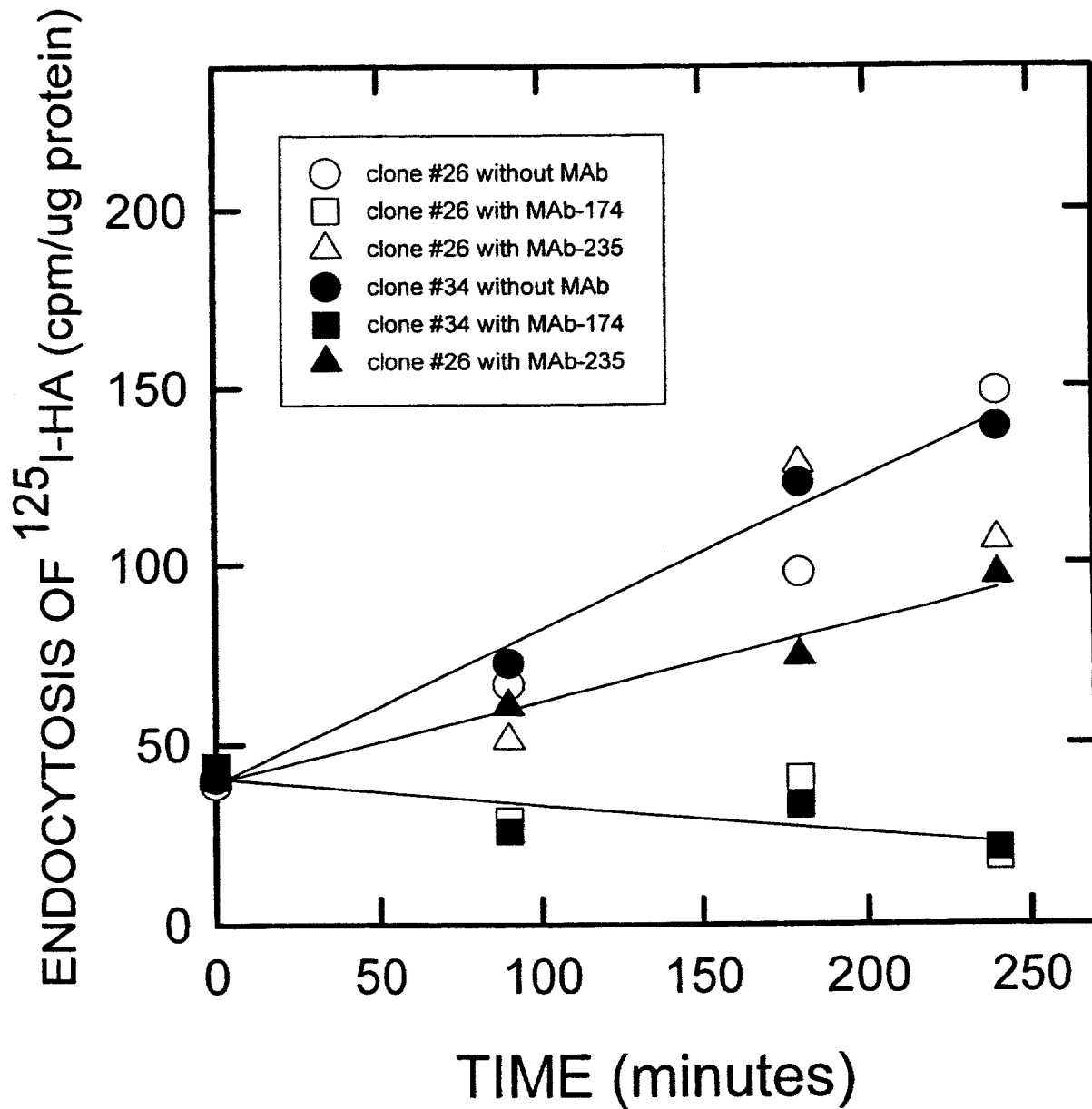


Figure 28

175SHARE 1 -----SLPS LLTRLEQMPD YSIFRGYIHH YNLASAIESA DAYTVFVPAN EAIENYIREK KATSLKEDIL RYHVVLGEBL LKNDLHNGMH RETMLGFSVL
 CAB61827 1111 LHLSQVLLP PRGDVPGQGG LLQQLDLVPA FSLFRELLQH HGLVPLQIEA TAYTTFVPTN RSLEA---QG NSSHLADATV RHHVVLGEL SMETLRKGGH RNSLLGPAHW
 BAA13377 754 LHLSQVLLP PRGDVPGQGG LLQQLDLV-A FSLFRELLQH HGLVPLQIEA TAYTTFVPTN RSLEA---QG NSSHLADATV RHHVVLGEL SMETLRKGGH RNSLLGPAHW

175SHARE 95 LAFFPLRNDQL YVNEAPINYT NVATDKGVH GLEKYLEIQ NRDNNDTII VRGEYKHSQ QAPPLETKP LRETRK---IY SIYFMGRSV FIGQPCQVR TITTRAWLA
 CAB61827 1218 IVFYNHSCQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRLHSHAEA LREKIVNTR RFRITQGFQL QDTPRKSIV RSGFSPSR---G SYTAK KIQVPLCPG
 BAA13377 861 IVFYNHSCQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRLHSHAEA LREKIVNTR RFRITQGFQL QDTPRKSIV RSGFSPSR---G SYTAK KIQVPLCPG

175SHARE 204 SLAHNAK PAP GEVK-MALG TASVWDGUNG TGTGOLGLF NGTAETETE GKYGIHQDA SVVHGRSQ GPLDGSIV DVGWGRVKID MEITTDNNG THTSANLL
 BAB15793 1 -----HLFGWS-DG TGVPEGEFG SGTAETETE GKYGIHQDA SVVHGRNQ GPLDGSIV DVGWGRVKID MEITTDNNG THTSANLT
 CAB61358 1 -----HLFGWS-DG TGVPEGEFG SGTAETETE GKYGIHQDA SVVHGRNQ GPLDGSIV DVGWGRVKID MEITTDNNG THTSANLT
 CAB61827 1224 FFGTLCPCP GGLGGV-S-G HQCCQDFLHG SGEHHEGF HGTAEEVEL GRYPNTGV DAHGLQOE GLQDGSIV NVGWOGLRD QKITSQPR KPDNANVQ
 BAA13377 967 FFGTLCPCP GGLGGV-S-G HQCCQDFLHG SGEHHEGF HGTAEEVEL GRYPNTGV DAHGLQOE GLQDGSIV NVGWOGLRD QKITSQPR KPDNANVQ

175SHARE 313 DPDGKAS K AAGFRNGTV TAINAETS NGSSTKAD KRTTPGNRV VKAGYTG DG IVLEINPL ENHGGDRNA EITQTGENQA VMLPKYTG DG-KVSLIN
 BAB15793 90 NSDGTAS K AAGFGQNGTI TAINAETS NGSSTKAD KRTTPGNRV VKAGYTG DG IVLEINPL ENHGGDRNA EITQTGENQA VMLPKYTG DG-KVSLIN
 CAB61358 3 EAVGTAS K AAGFGQNGTI TAINAETS NGSSTKAD KRTTPGNRV VKAGYTG DG IVLEINPL ENHGGDRNA EITQTGENQA VMLPKYTG DG-KVSLIN
 CAB61827 1433 DSAGAST A AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPQRT TQDGYMGD ELQEINSL IHGGCHIA EIPTGQQV SSSREGYSG DGIRTELD
 BAA13377 1076 DSAGAST A AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPQRT TQDGYMGD ELQEINSL IHGGCHIA EIPTGQQV SSSREGYSG DGIRTELD

175SHARE 422 VLTNNGGS PFAPNYTEQ DQRIITKPD Y-TGDGIVR GSIYGELEPN PSTSQYFFQL QEHAVRELAG PGFTTFVAP--LSSSFNHE PRKDWQDQG IMSQVLYRHV
 BAB15793 199 VLTNNGGS EFALNHGQ VERTITKPN Y-IGDGTFR GSIYGELEPN PSTSQYFFQL QEHFVKDLVG PGFTTFVAP--LSAAFDEE ARKDWIKYG LMPQVLYRHV
 CAB61358 112 VLTNNGGS EFALNHGQ VERTITKPN Y-IGDGTFR GSIYGELEPN PSTSQYFFQL QEHFVKDLVG PGFTTFVAP--LSAAFDEE ARKDWIKYG LMPQVLYRHV
 AAF82398 1 -----VLTNNGGS PFAPNYTEQ DQRIITKPD Y-TGDGIVR GSIYGELEPN PSTSQYFFQL QEHAVRELAG PGFTTFVAP--LSSSFNHE PRKDWQDQG IMSQVLYRHV
 CAB61827 1543 VLTNNGGS PYATKSTGD QRTITKPD HTVGDGLTR ARVGLGLRD KHAS--FFSL RLLEYKELKG DGFTTFVAP ADLMSNLSD ELARIRAHQ L--VFRYHV
 BAA13377 1186 VLTNNGGS PYATKSTGD QRTITKPD HTVGDGLTR ARVGLGLRD KHAS--FFSL RLLEYKELKG DGFTTFVAP ADLMSNLSD ELARIRAHQ L--VFRYHV

175SHARE 528 VGLQLLN LKVTTSATLL QGEPVSVSVS QDTVFINNEA KVLSSDIIST NGVIHIDKL LSPKNLLITP KDALGRVLQN LTTVAANHGY TKFSKLIQDS GLLSVITDSI
 BAB15793 305 VAHQLLLEN LKLISNATSL QGEPVSVSVS QSTVYINNA KIISSDIIST NGVIHIDKL LSPKNLLITP KDNSTRILQN LTTATNNGY IKFSNLQDS GLLSVITDPI
 CAB61358 218 VAHQLLLEN LKLISNATSL QGEPVSVSVS QSTVYINNA KIISSDIIST NGVIHIDKL LSPKNLLITP KDNSTRILQN LTTATNNGY IKFSNLQDS GLLSVITDPI
 AAF82398 10 VAHQLLLEN LKLISNATSL QGEPVSVSVS QSTVYINNA KIISSDIIST NGVIHIDKL LSPKNLLITP KDNSTRILQN LTTATNNGY IKFSNLQDS GLLSVITDPI
 CAB61827 1648 VGRRLRSED LLBQYATALL SGHPLRFSE EGSYILNDA RVSSDHEAV NGIHLIDRV LLPEALHWE PDDAPIPRN VTAAGQGFY KIFSGLLKVA GLPLLLREAS
 BAA13377 1291 VGRRLRSED LLBQYATALL SGHPLRFSE EGSYILNDA RVSSDHEAV NGIHLIDRV LLPEALHWE PDDAPIPRN VTAAGQGFY KIFSGLLKVA GLPLLLREAS

175SHARE 638 HTFVTWFMT DKALEALPE QDQFLFNQDN KDKLSYLFK HVIRDSKALA SLPASASWK TLQSGELSVR GTGSDIGEL FLNQCMRFI HRGLLFDVGV AYGIDLLM
 BAB15793 415 HTFVTWFMT DQALHALPAE QDQFLFNQDN KDKLKEYLFK HVIRDAKULA VDLPTSTAMK TLQSGELSVK GAGRDIGDL FLNQCMRFI QRELLFDLGV AYGIDLLD
 CAB61358 328 HTFVTWFMT DQALHALPAE QDQFLFNQDN KDKLKEYLFK HVIRDAKULA VDLPTSTAMK TLQSGELSVK GAGRDIGDL FLNQCMRFI QRELLFDLGV AYGIDLLD
 AAF82398 120 HTFVTWFMT DQALHALPAE QDQFLFNQDN KDKLKEYLFK HVIRDAKULA VDLPTSTAMK TLQSGELSVK GAGRDIGDL FLNQCMRFI QRELLFDLGV AYGIDLLD
 CAB61827 1758 HRPTMLWPT DAAFRALPPD RQAWLYHEDH KDKLAALLRG HMTRNVEALA SLPNLGPR LR TMGTPISEFS SRTRP-GEL MVGEDDARIV QRHLPEBGL AYGIDQLEP
 BAA13377 1401 HRPTMLWPT DAAFRALPPD RQAWLYHEDH KDKLAALLRG HMTRNVEALA SLPNLGPR LR TMGTPISEFS SRTRP-GEL MVGEDDARIV QRHLPEBGL AYGIDQLEP

175SHARE 748 PTLGGRDTF TTFDIP-GE GSITFTPK P LKSPKPGVK K--LY-----NLPF R-----RNVE-G QNLTVVIQT PRKHGYFMP DQA PGGP
 BAB15793 525 PTLGGRDTF TTFDAS-GE GSIVNTPS P RWSKPKGVK K--LY-----NLPF R-----RNLE-G RERSLVIOI PRKHGYFMP DQA PGGP
 CAB61358 438 PTLGGRDTF TTFDAS-GE GSIVNTPS P RWSKPKGVK K--LY-----NLPF R-----RNLE-G RERSLVIOI PRKHGYFMP DQA PGGP
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 CAB61827 1867 PTLGGRDTF ETPLRLANT SI GLEPP P BGSQBGSPSE AWRPYKFW TSPPLHSLGL RSVVHPSLV GRPQGLGRG HRNVTITWK PSKHGYGS EQA PGGP
 BAA13377 1510 PTLGGRDTF ETPLRLANT SI GLEPP P BGSQBGSPSE AWRPYKFW TSPPLHSLGL RSVVHPSLV GRPQGLGRG HRNVTITWK PSKHGYGS EQA PGGP

175SHARE 833 TPNRNGMRL DLYTFMGQL HTGFNGTA ELWHGRFPG DQPRSEH GQDEGITGS GELITGWT AASDTPTAV FAVTTPA SV HATKENNT VNLNYESGD
 BAB15793 609 APNRRGVLL DQYSATGEK HTGFNGTA ELWHGRFPG DQPRSEH GQDEGITGS GELITGWT GPSDTQAVL PAVTTPA SV HATKENNT ENLDYESGD
 CAB61358 522 APNRRGVLL DQYSATGEK HTGFNGTA ELWHGRFPG DQPRSEH GQDEGITGS GELITGWT GPSDTQAVL PAVTTPA SV HATKENNT ENLDYESGD
 AAF82398 314 APNRRGVLL DQYSATGEK HTGFNGTA ELWHGRFPG DQPRSEH GQDEGITGS GELITGWT GPSDTQAVL PAVTTPA SV HATKENNT ENLDYESGD
 CAB61827 1977 SPSDRGVM DQMSGSGQL RSGFAGTA ELAPGAFPG HQACRIVH GRDEGLGGS GSFDGWT GPRVQLEL QPVTPP AP EAVRAGNS ESLYESGD
 BAA13377 1620 SPSDRGVM DQMSGSGQL RSGFAGTA ELAPGAFPG HQACRIVH GRDEGLGGS GSFDGWT GPRVQLEL QPVTPP AP EAVRAGNS ESLYESGD

175SHARE 943 ITTVVDH KQNGGAKVA KRSQGTQVS SSKGYKGD GYSLEIDF ADGVNGGHE HATRMITGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHPDAS
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 CAB61358 632 ITTVVDH KQNGGAKVA KRSQGTQVS SSKGYKGD GYSLEIDF ADGVNGGHE HATRMITGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHPDAS
 AAF82398 424 ITTVVDH KQNGGAKVA KRSQGTQVS SSKGYKGD GYSLEIDF ADGVNGGHE HATRMITGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHPDAS
 CAB61827 2087 RVTIVADLQ DGHGGESEHA NISQVGMVT TLPDYEGD GWSRARNF TDGHRGGESE HANLSTGLN TRREHAGY VGDGLN-EP EQLPIDRLQ DNGQHPDAS
 BAA13377 1730 RVTIVADLQ DGHGGESEHA NISQVGMVT TLPDYEGD GWSRARNF TDGHRGGESE HANLSTGLN TRREHAGY VGDGLN-EP EQLPIDRLQ DNGQHPDAS

175SHARE 1052 ADLYFQDIT VGVFHLRSPL GQYKLTFDKA REAANEAAAT IATYNQLSYA QKAKYHLSA GWLESGRVAY PTTFASQNG SGVVGIVDYG PRANKSEMD VFRYMKDVN
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 BAA13377 1840 TDQHFQEK R AGVFLQATS GPYGLNFSEA EAAEAGGAV LASFPQLSAA QQLGFHLLM GWLANGSTAH FVVPFVAD GNGRVGIVSLG ARKNLSERWD AYFRVQDVA

175SHARE 1162 TKAGYVGD GFS-SGNLL QVMSFPPSLT NFLTVEVLA FS KSSARGAFL KHLTDLISRG TLFVPQNSGL PGKSLSGRD IEHLINNVN SFYNDLVNLT FLRTMLGSQL
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 BAA13377 1950 TRRNGFVGD GISTNGKLL DVLAATANFS TFGMLLGYA NATQRLDFL DFLDELTYK TLFVPVNEG FVDMTSLGPD LELHASNATL LSAN-ASQK LLPAHSGLSL

175SHARE 1271 LITFS--QD QLHQ-ETRFV DGRSILQWDI IAANGILHII SEPLRAPPTA ATA---AHSG LGTGIRCAV LVTGALA--L AYSYFRIK RTTG--FQRF DQKRTLMWL
 BAB15793 1047 LITAS--QD PLOPTETRFV DGRAILQWDI PASNGIHHVI SRPLKAPPAP VTL---THGT LGAGIFFAI LVTGAVA--L AYSYFRIK RTTG--FQRF ESEEDINVA
 CAB61358 924 LITAS--QD PLOPTETRFV DGRAILQWDI PASNGIHHVI SRPLKAPPAP VTL---THGT LGAGIFFAI LVTGAVA--L AYSYFRIK RTTG--FQRF ESEEDINVA
 AAF82398 752 LITAS--QD PLOPTETRFV DGRAILQWDI PASNGIHHVI SRPLKAPPAP VTL---THGT LGAGIFFAI LVTGAVA--L AYSYFRIK RTTG--FQRF ESEEDINVA
 CAB61827 2416 IISDAGPNS SWAPVAPGV VVSRILVWDI MAFNGIHAL ASPLLAPQP QAVLAPEAPP VAAGV--GAV LAAGALLGLV AGAILXLRAG KFMGPFSAF QAEDDADD
 BAA13377 2059 IISDAGPNS SWAPVAPGV VVSRILVWDI MAFNGIHAL ASPLLAPQP QAVLAPEAPP VAAGV--GAV LAAGALLGLV AGAILXLRAG KFMGPFSAF QAEDDADD

175SHARE 1370 LASSP-RIS QTLCMRPQR HPQSPPVTPS QTLENRIWRT ATLGWCHGPD MRSQATTVT VFR
 BAB15793 1147 LGKQPPNIS NPLY-ESTTS APPEPSYDPF TDSER-----QLEGNDF LRTL
 CAB61358 1024 LGKQPPNIS NPLY-ESTTS APPEPSYDPF TDSER-----QLEGNDF LRTL
 AAF82398 852 LGKQPPNIS NPLY-ESTTS APPEPSYDPF TDSER-----QLEGNDF LRTL
 CAB61827 2524 SPWQ-EGTN-PTLVSVNPFV FGSDFCEFP DD-----SLEEDFPD TQRLITVK--
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Figure 29

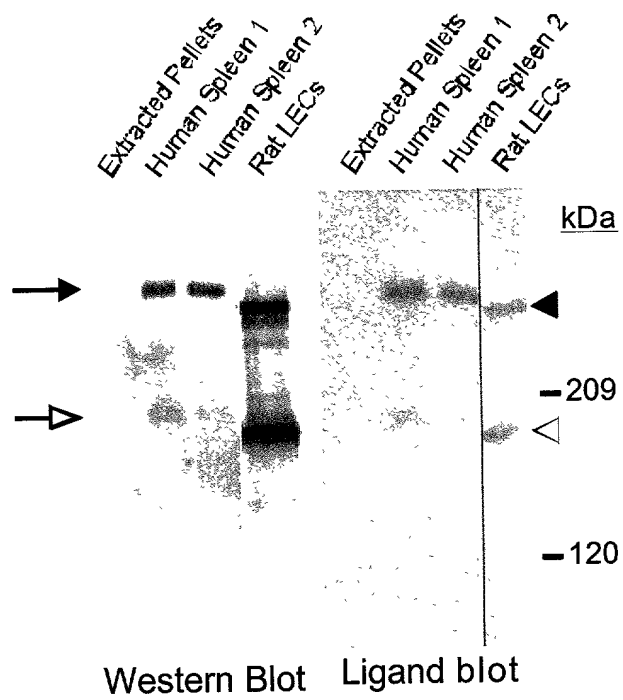


Figure 3 0

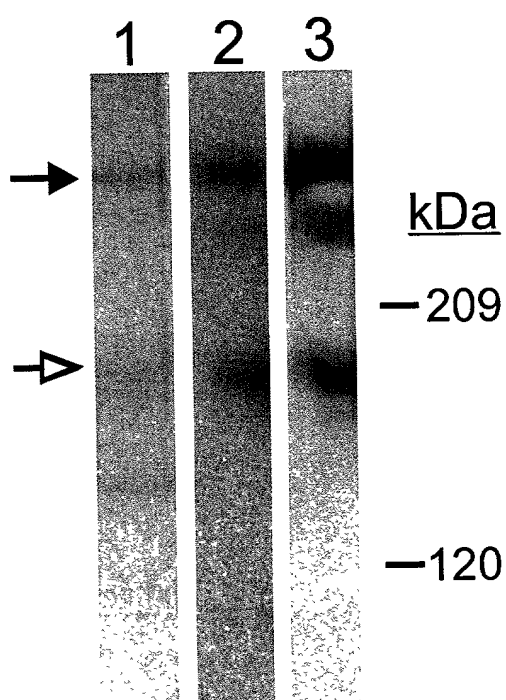


Figure 31

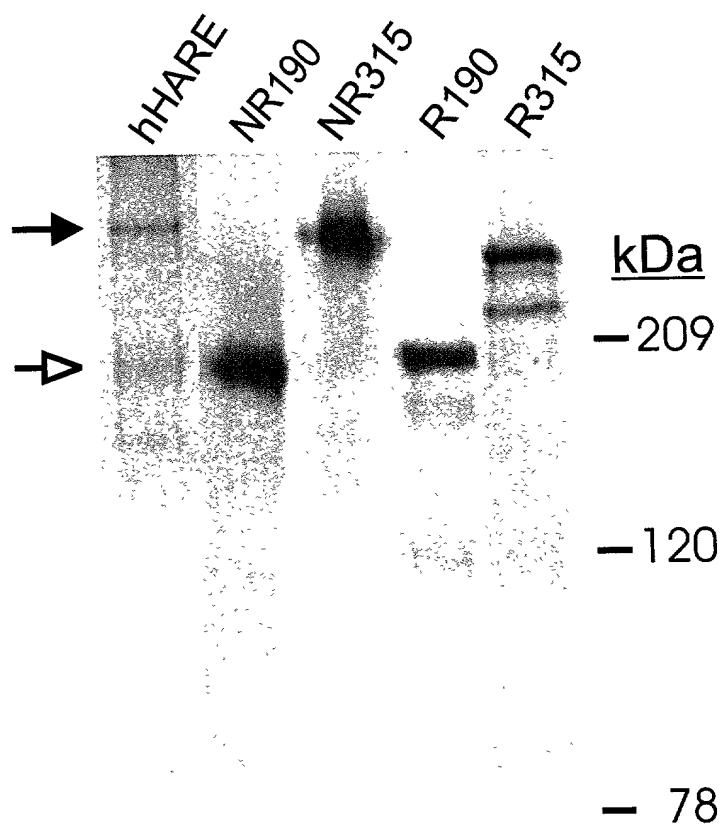


Figure 3 2

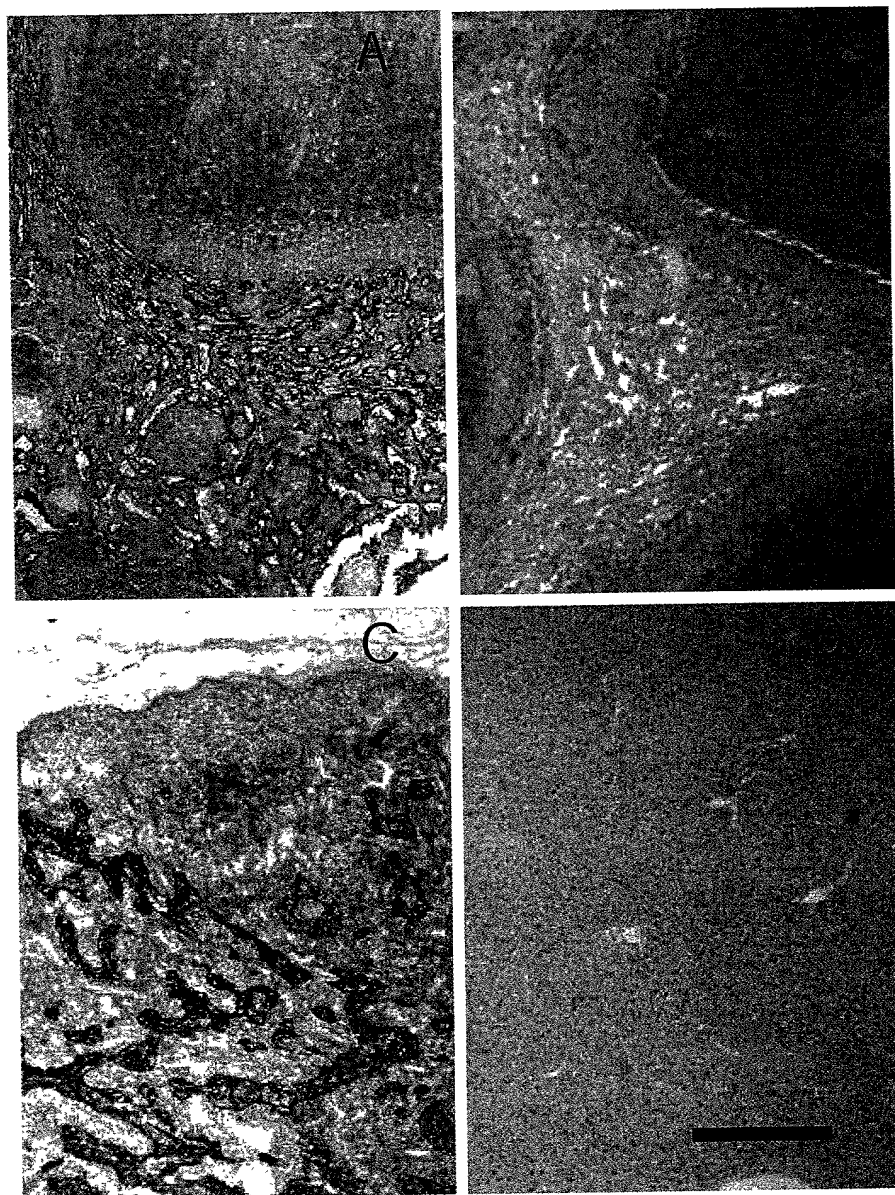


Figure 33

1 ATTCAATATAACTTGGCGGAATGCAATTAGGCTTGCCCATGCCACAGTTGTTCCTCAAACAACAACTGCCTCAGAGAATTACATCAGGGAGAAGAAAGTCTTGCTCTAGAGGAGGAC
I Q Y N L A N A I E A A D A Y T V F A P N N N A I E N Y I R E K K V L S L E E D

121 GTCTCCCGGATCATGTGGTCTGGAGGAGAACTCCTGAAGAATGACCTGCACATGGCATGCATGTGAGCCATGTGGTGTCTCTTCTTAGCTTCTTCTCCAATAATGAC
41 V L R Y H V H V L E E K L K N D L H N G M H R E T M L G F S Y F L S F L H N D

241 CAGCTCTATGTAAATGAGGCTCCAATAAATAACCAATGTAGCCACTGATAAGGAGTGTATCCATGGCTTGGGAAATTTCTTGGAAATTCAGAAAGACAGATGTGTAATAATGACACT
81 Q L Y V N E A P I N Y T N V A T D K G V I H G L G K V L E I O K N R C D N N D T

361 ACTATTATACGAGGAAGATGTAGGACATGCTCCCTCAGCTGACCTGCCACTTCGAAGTAACTCTAGNATGAGAAAGAGGATGCATCTACTCTTACTCTGGGAGGACGA
121 T I R Y H V R C R T C T C S E L T C C P F G T K S L G N E K R R C I Y T S Y F M G R R

481 ACCCTGTTTATTTGGGTGCCAGCCAAATGTGTGAGAACCTCATTACGAGAGAATGCTGTGCGGCTTCTTGGCCCCAATGCCAGCCCTGCCAGGAATGCCAGAAATGCTGCTTT
161 T L F I G C Q P K C V R T V I T R E C C A G F G P Q C Q P C P G N A Q N V C F

601 GGTAATGGCATCTGTGTGAGTGAATGAGTGTGTGTGTGTGGGAGGGCTCAGCGGCACAGCCTGCGAGACCTGCACCGAGGGCAAGTACGGCATCCACTGTGACCAA
201 G N G I C L D G V N G T G V V C E C G E G F S G T A C E T C T E G K Y G I H C D Q

721 GCATGTCTTGTGTGAGGAGATGCAACCAAGGACCCTTGGAGATGDCCTGTGTGATGTGTGGTGGCGAGGAGTGCATTTGTGCAATGCAACCAAGAGAACTGCAAT
241 A C S C V H G R C N C G P L G D G D G S C D C D V G W R G V H C D N A T T E D N C N

841 GGGACATGCCATACCGAGCCAACTGCCTCACCACTGATGGTGTGACAGCTTCTGCAAGTGTGAGCAGGATTCCAAGGAAACGGGACCATCTGCACAGCAATCAATGCCTGTGAGATC
281 G T C G H T S A N R C C T L T N S D G T A S D G C A A G F Q G N G T I C T A I N A C E I

961 AGCAATGGAGGTGTCTGCAAGGCTGACTGTAAAGAAACCCAGGAGGCGAGTGTGCACTGCAAGGAGGCTACAGGCTACAGGCTGTGCTGGTGAATGTGCTGGAAATCAACCGGTGT
321 S N G G C S A K A D C K R T T P G R R V C T C K A G Y T G D G I V C L E I N P C

1081 TTGAGAACCATGGTGGCTGTGACAAGAATGCGGAGTGCACACAGACAGGACCCAAACAGGCTGCTGTAACTGTTTGGCAGCATACACTGAGAGTGAAGAGGCTGCACACTCATCAAT
361 L E N H G G C D K N A E C T Q T G P N Q A A C N C L P A Y T G D G K V C I L N

1201 GTCTGCTTAACTAAAAATGGCGGCTGTAGTGAATTTGCCATCTGCACCAACCATGGGACAGTGAAGAGTGTGATTCGAAGCAAACTACATTTGAGATGGATTACCTGCCGGGAGG
401 V C L T K N G G C S E F A I C N H T G Q V E R T C T C K P N Y I G D G F T C R G

1321 AGCATTATCAGGAGCTTCCCACCAACCCGAAAACCTCCAGTATTTCTCCAGTGTGAGGAGCATTTCTGGAASATCTGGTGGGCGGCGCCCTCAGTTGTTTGCACCTTTATCT
441 S I Y Q E L P K N Q Y F F Q L Q E H F V K D L G V G P G P F T V F A P L S

1441 GCAGCCTTTGATGAGGAAGCTCGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTCGATACATGTGGTGGCTGCCACAGCTGCTTCTGGAAACCTGAAATTGATC
481 A A F D E E A R V K D W D K I Y G L M P Q V L R Y H V V A C H Q L L E N L K L I

1561 TCAATGCTACTTCCCTCAAGGAGCCCAATAGTCTCCGCTCTCTCAGAGCAGGCTGTATATAACAATGAAGCTAAAGTACATATCAGTACTAATGGGATGTGT
521 S N A T S L Q G E P I V I S V S Q S T V Y I N N K A K I I S S D I I S T N G I V

1681 CATATCATAGACAAATGTCTATCTCCCAAAATTTGCTTATCACTCCCAAGACAACCTGGAAGAAATCTGCAAAATCTACGACTTTGGCAACAAACATGGGTACATCAATTTAGC
561 H I I D K L L S P K N L L I T P K D N S G R I L Q N L T T L A T N N G Y I K F S

1801 AACNTAATACAGGACTCAGGTTGTGCTGAGTGTATCCAGTCCATCCACCCAGTCACTCTCTTGGCCACCGCAAGCCCTCATGCCCTACCTGCTGAACAACAGGACTTC
601 N I I Q D S G L L S V I T D P I H T P T D Q A L H A L P A E Q Q D F

1921 CTGTTCAACCAAGACAACAGGACAAGCTGAAGGAGTATTGAATCTTCTGATGTATGAGTGAAGTGTAGCTTGTGGATCTTCCCACATCCACTGCCTGGAAACCTTCAAGGT
641 L F N Q D N K D K L K E Y L K I F H V I R D A K V L A V D L P T S T A W K I L Q G

2041 TCAGCTGAGTGTGAATGTGGAGCTGGCAGGACATCCGTCAGCTCTTCTGAATGGCCAAACCTGCAGAAATGTGCAGCGGAGCTCTTGTGACCTGGGTGTGGCTACGGCATT
681 S E L S V K I C G A G R D I G D L F L N G Q T C R I V Q R E L L F D L G V A Y G I

2161 GACTGTCTGCTGATTCACCCACTTGGGGGCGGCTGTGACACCTTTACTACTTTCGATCGCTCGGGGAGTGTGGGAGCTGTGTCAATATCCCFAGTSCCCAAAGTWSAKKP
721 D C L L I D P T T L G G R C D T F T T C T D A S G G E G S C V N T

2281 AAGGTGTGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGGAGCGGTGCAGCTTGTGTATCAGATCCCAGGTGCTGCAAGTGTCTTCTGGGCA
761 K G V K Q K C L Y N L P F K R N L E G C R E R C S L V I Q I P R C K I G Y F R G

2401 GACTGTCAAGGCTGCTGGAGGAGCAGATGCCCTGTAATAAACCAGGAGTGTCTGCTGATCAGTCTCGGCCACGGAGGTGAATGCAACACCGGCTTCAATGGGACGGGTGT
801 D C Q A C P G G P D A P C T N A R C G G T V C L D Q Y S A T G : E C K C N T G F N G T A C

2521 GAGATGTGCTGGCGGGAGATTGGGCTGATTTGTCTGCGCTGTGCTGCAGACCGGACGTGOGATGTGGCATCCAGGCTCCGGGCACTGGCTCTGTGAAACGGGTGGACA
841 E M C W P G R F G P G L F C G C S D H G C C D D G I T G S G Q C L C T E T G W T

2641 GGCCCTCGTGTGACATCAGGAGTTTTGCTGCGAGTGTAGCGCTCTTGTGTCTGCTCATGCCACCTGTAAGGAGAAACAACGCTGTGAGTGAATCGGATTATGAAGGTGACGGA
881 G P S C D T Q A V L P A V C T P P C S A H A T C K E N N T C E C N L D Y E G D G

2761 ATCACTGCACAGTTGTGGAATTTCTGCAACAGGACAACGGGGCTGTGCAAGAGTGGCCAGATGCTCCAGAAAGGCGACGAAGGTCTCTGACAGCTGCCAGAGGATACAAAGGGAC
921 I T C T V V D F C G Q D N G G C A K V A R C S Q K G T K V S C S C Q K G G I

2881 GGGCAGCTGCACAGAGATAGACCCCTGTGAGACGGCTTAAACGAGGGTGTGACGAGCAGCCACCTGTAAGATGACAGGCGCGGCAAGCAAGTGTGAGTGAATAAGTCACTAT
961 G H S G S T E I D P C A D G L N G G C H E H A T C K M T G P G K H K E C K S H Y

3001 GTCCGAGATGGGCTGAATCTGAGCGGGAGCTGCCCATTTGACCGTCTTACAGGACAATGGGAGTGCATGCAGACGCAAAATGTGCACTTCCACTTCCAGGATACCACTGTT
1001 V G D G L L N C E P E Q L P I D R C L Q D N G Q C H A D A K C V D L H F Q D T T V

3121 GGGGTGTTCCATCTACCTTCCCACTGGGCGAGTAAAGTGTGACTTGTGACAAACCGAGAGGCTGTGCCAACGAGCTGGCAGCATGGCACTTCAACAGCTCTCTTATGCCAG
1041 G V F H L R S E L G Q Y L L E D K A R I E A C N A E A T M A T Y Q L S Y A Q

3241 AAGGCAAGTACCACTGTGCTCAGAGCTGGCTGGAGACCGGGGGTGTGCTACCCCAAGCTTGCCTCCAGAACTGTGGCTCTGTGTGGTGGGATAGTGGACTATGGACCT
1081 K A K Y H L C S A G W L E T G R V A Y P T A F A S Q N C G S G V V G I V D Y G P

3361 AGACCAACAGAGTGAATGTGGGATGTCTTCTGCTATCGGATGAAGAGTGAATCTGCACTGCAAGGTGGGCTATGTGGAGATGGCTTCTCATGTGAGGGAACCTGTGAGGTC
1121 R P N K S E M W D V F C Y R M K D V N C T C K V G Y V G D G F S C S G N L L Q V

3481 CTGATGTCTTCTCCCTCACTCACAACCTTCTGAGCGGAAGTGTGCTGCTTATTCACAGCTCAGCTCAGAGGCGGTGCATTTCTAGAACCTGACTGACCTGTCCATCCGGGACCTCT
1161 L M S F P S L T N F L T E V L A Y S N S S A R G R A F L E H L T D L S I R G T L

3601 TTTGTGCCACAGACAGTGGGCTGGGGGGAATGAGACTTGTCTGGCGGACATCGAGCACCTCGCCAACTGTGAGCTTCTTCTCAATGACCTTGTCAATGGCACCACCTG
1201 F V P Q N S G L G E N E T L S G R D I E H H L A N V S M F F Y N D L V N G T T L

3721 CAAACGAGGCTGGGAAGCAAGTGTCTCATCTGACCCAGGAGCCACTCCAACGAGCGGAGACAGGTTGTGTGATGGAAGAGCATTCTGCAAGTGGGACATCTTGTGCTCAATGGG
1241 Q T R L G S K L L I T A S Q D P L Q P T E T R F V D G R A I L Q W D I F A S N G

3841 ATCATCTGTCTTCCAGGCTTTAAAGACACCCCTGCCCGTACCTTGACCCCACTGTGCTGGGAGCAGGATCTTCTTGGCATCATCTGGTGTGAGTGGGCTGTTGCTGTG
1281 I I H V I S R P L K A P P A P V T L T H T G L G A G I F F A I I L V T G A V A L

3961 GCTGCTTACTCTACTTTCGGATAAACCGGAGAAACATCGGCTTCCAGCATTTGTAGTCCGAAGGACATTAATGTTCAGCTTGTGCAAGCAGCAGCCTGAGAATATCTCGAAGCCC
1321 A A Y S Y F R I N R T I G F Q H F E S E E D I N V A A T L G K Q Q P E N I S N P

4081 TTGTATGAGAGCAACCTCAGCTGCCCCAGAACCTTCTACGACCCCTTACGGACTCTGAAGAACGGCAGCTTGAAGGCAATGACCCCTTGAGGACACTGTGAGGGCTGGACGGGAG
1361 L Y E S T T S A P P E P S Y I D P F T D S E E R Q L T E G N D P L R T * (1394aa)

4201 ATGCCAGCATCACTCACTGCCACTGGGCGCACTCAACTGTGAATCTCAGCAGGAGTGTGCTTTTAGGAACGCTAAAGCTCTTAAAGCAGTCAAGAGCCATCACTCTCTGGTGTGAT
4321 CTGGGGGTTGTTTCTGTGGGTGAGAGATGTGTGCTGTGCCAACAGGACAGCTTCTGACCT

[illegible]

hHARE	1	IQYNLANAIEAADAYTVFAP	NNNAIENIYIREKKVLSLEED	VLRYHVVLKLLKNDLHNG	MHRETMGLGFSYFLSFLFLHND	QLYVNEAPI	INVTADTKGV
rHARE	23	IHYNLASAIESADAYTVFVP	NNEAIENIYIREKKATSLKED	ILRYHVVLGKLLKNDLHNG	MHRETMGLGFSYLLAFLRLND	QLYVNEAPI	INVTADTKGV
hHARE	101	IHGLGKVLKIQNR	DNND	TIIRGR	RT	SSELT	PFGT
rHARE	123	IHGLEKVLKIQNR	DNND	IIIVRGE	GK	SOQAP	PLET
hHARE	201	GNGICLDGVNG	GV	E	GEG	FSGTA	ET
rHARE	222	GTASVWDGVNG	GT	Q	GLG	FNGTA	ET
hHARE	301	AAGFQNG	II	TAINA	EI	SNGG	SAKAD
rHARE	322	AAGFRNG	GV	TAINA	ET	SNGG	STKAD
hHARE	401	VLTKNNG	SEFAI	NYT	Q	VERT	TI
rHARE	422	VLTNNNG	SPFAF	NYT	Q	DQRI	TI
hHARE	501	VLRYHVVA	HOLLENLKLI	SNATSLQGEPIVISVSQSTV	FINNEAKVLSDDIISTNGIV	YINNKA	LISSDIISTNGIV
rHARE	522	VLRYHVVG	QQLLLDNLKVT	TSATTLQGEPIVISVSQDTV	FINNEAKVLSDDIISTNGIV	HVIDKLL	SPKNLLITPKDAL
hHARE	601	NLIQDSGLSVITDPIHTPV	TLFWPTDQALHALPAEQQDF	LFNQDNKDKLKEYLKFHVIR	DAKVLAVDLPTSTAWKTLOQ	SELSVK	GAGRDIGDLFLNG
rHARE	622	KLIQDSGLSVITDPIHTPV	TVFWPTDKALEALPPEQQDF	LFNQDNKDKLKEYLKFHVIR	DAKVLAVDLPTSTAWKTLOQ	SELSVK	GAGRDIGDLFLNG
hHARE	701	QT	RIVQRELLFDLGVAYGI	D	LLIDPTLGR	DTFTTFD	ASGE
rHARE	722	QM	RFIHRGLLFDVGAYGI	D	LLMNPTLGR	DTFTTFD	IPGE
hHARE	800	RD	QA	PGGPDAP	NNRGV	LDQYSATGE	K
rHARE	822	PD	QA	PGGPDTP	NNRGM	RDLYTPMGQ	L
hHARE	900	AHAT	KENNA	E	NLDYEGD	GIT	TVVDF
rHARE	922	VHAT	TENNA	V	NLNYEGD	GIT	TVVDF
hHAR	1000	YVGDGLN	EPEQLPIDR	LQ	DNGQ	HADAK	VDLHFQDIT
rHARE	1022	YVGDGVD	EPEQLPLDR	LQ	DNGQ	HPDAS	ADLYFQDIT
hHARE	1100	PTAFASQN	SGSVVGI	VDYX	PRPN	SEMWDVF	YRMKDVN
rHARE	1122	PTTYASQK	GANVVGI	VDYX	SRAN	SEMWDVF	YRMKDVN
hHARE	1200	LFVPQNSGLGENETLSGRDI	EHHLANVS	SMFFYN	DLVNGT	EHHL	TNVNVSFYN
rHARE	1222	LFVPQNSGLPGNKLSGRDI	EHHLTNVN	VSFYN	DLVNGT	EHHL	TNVNVSFYN
hHARE	1300	HTGLGAGIFFAILI	VTGAVA	LAAYSYFR	INRR	TIG	FOHFE
rHARE	1321	HSLGTGIFCAVVLVTGAIA	LAAYSYFR	INRR	TIG	FOHFE	FOHFE
rHARE	1421	SOQATTVTVP					

Figure 36

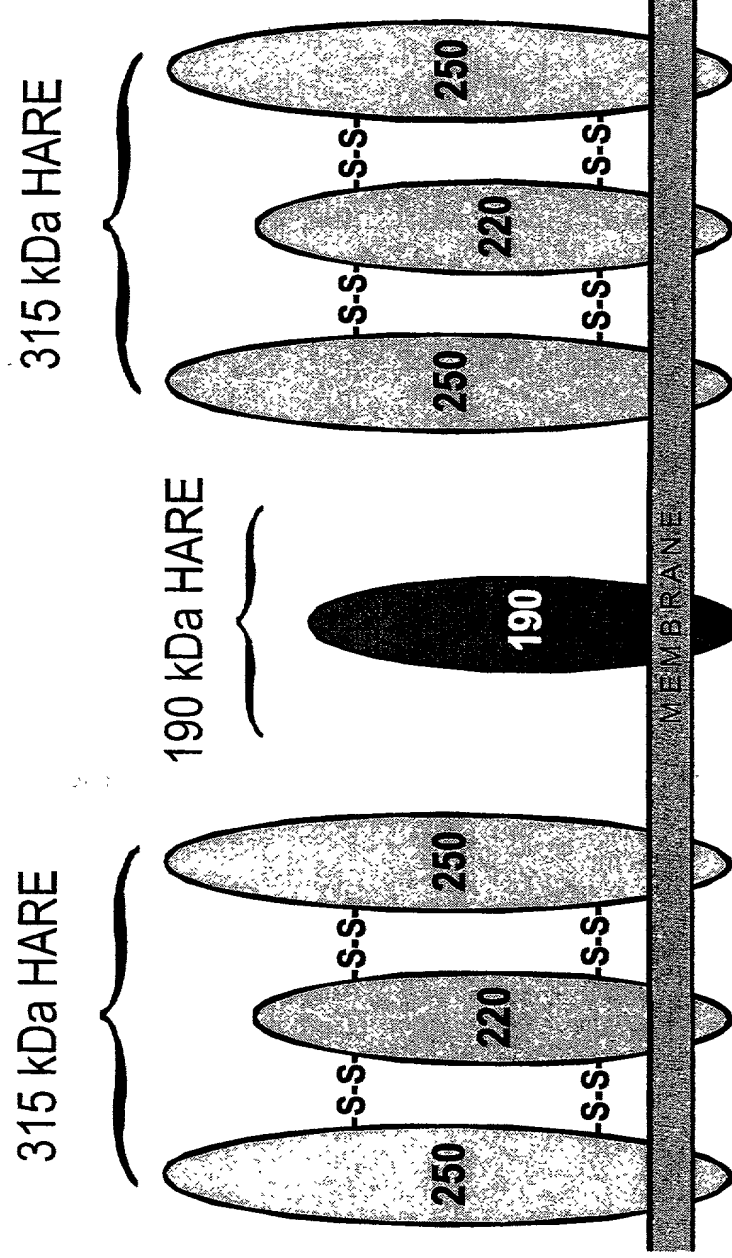


Figure 37

Amplification of the 1394 amino acid HARE
Open Reading Frame from a human lymph
node cDNA Library

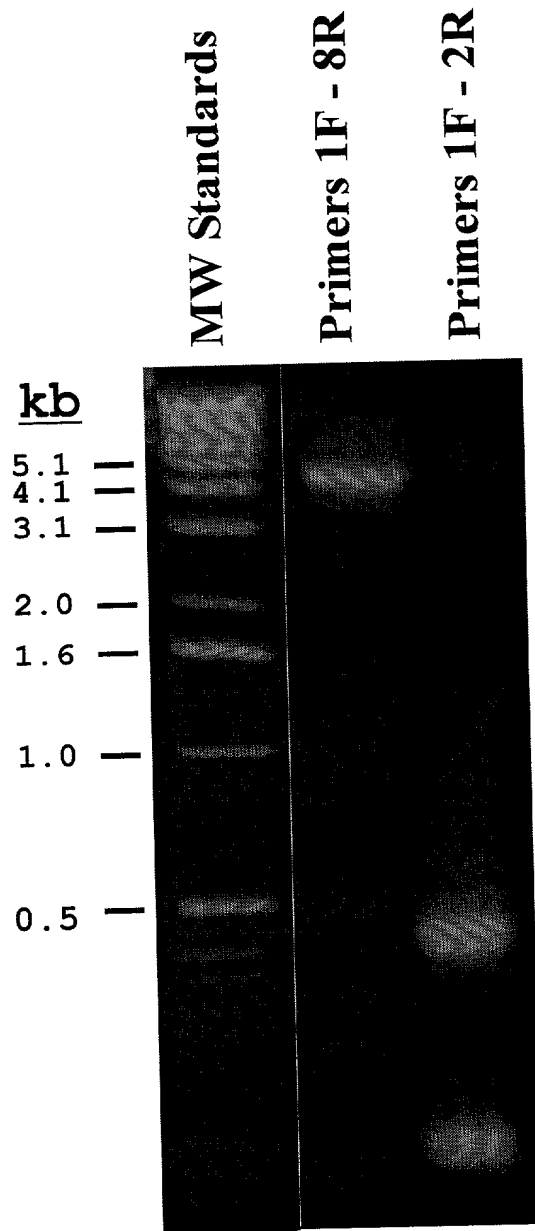


Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)

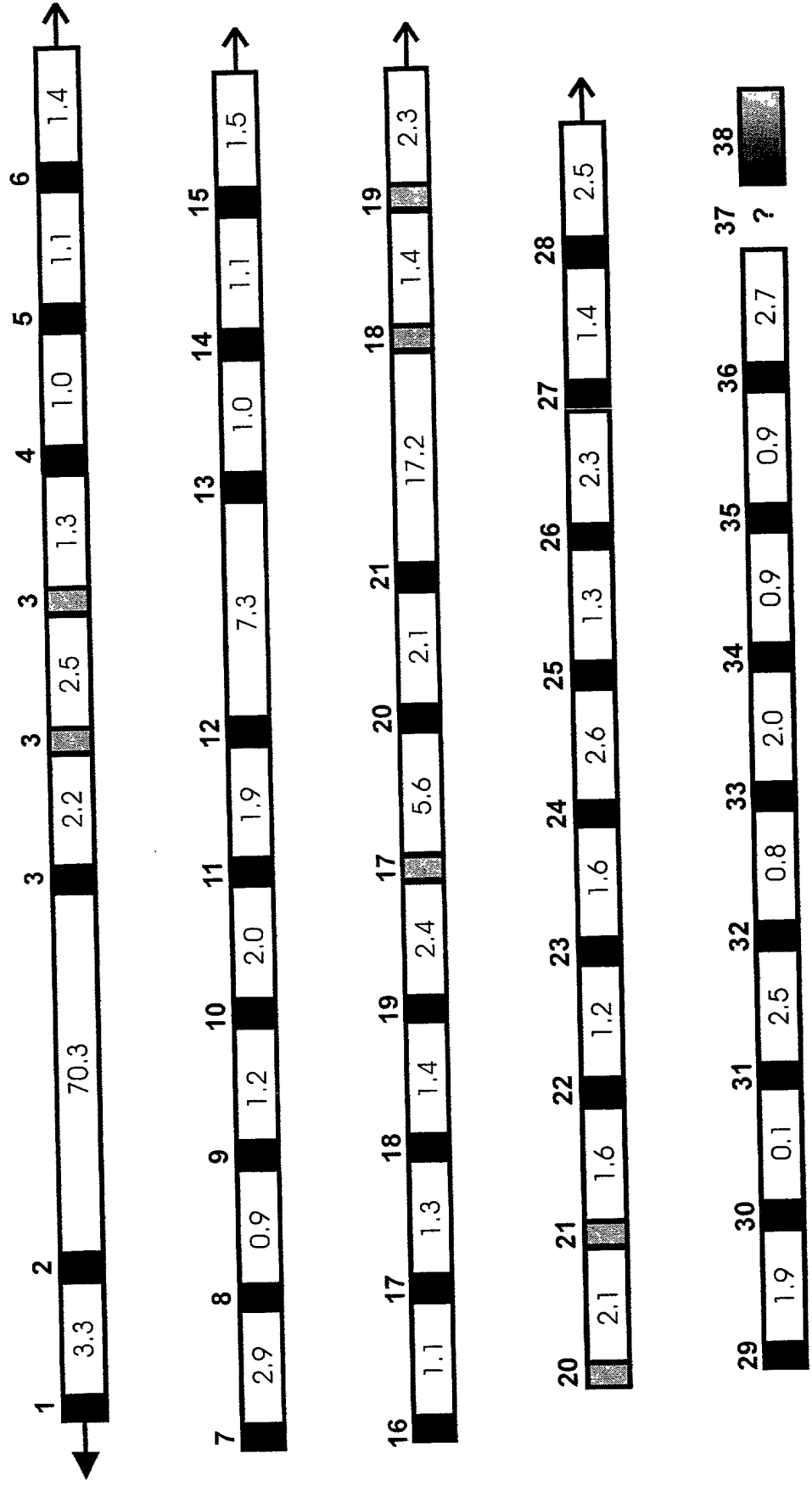


Figure 3 9

